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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: June 15, 2003, 18:20:48 ; Search time 1282 Seconds  
(without alignments)  
9874.977 Million cell updates/sec

Title: US-09-884-987-1\_COPY\_765\_1199  
Perfect score: 435  
Sequence: 1 aagagaaggaagtagtacagaa.....atgaaatccaaagcttggtc 435

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.om.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sv.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*  
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30: em.htg\_hum.\*  
31: em.htg\_inv.\*  
32: em.htg\_other.\*  
33: em.htg\_mus.\*  
34: em.htg\_pln.\*  
35: em.htg\_rod.\*  
36: em.htg\_nam.\*  
37: em.htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	435	100.0	698	9	HSPASCD3	247995 H.sapiens F
2	435	100.0	761	9	HSPASCD3	247994 H.sapiens F
3	435	100.0	836	9	HSPAS46DL	270520 H.sapiens F
4	435	100.0	857	9	HSPAS346	X83491 H.sapiens m
5	435	100.0	899	9	HSPAS4DEL	X70519 H.sapiens F
6	435	100.0	920	9	HSPAS34	X83490 H.sapiens m
7	435	100.0	945	9	HSPASCD31	247993 H.sapiens F
8	435	100.0	1008	6	E05336	E05336 DNA encodin
9	435	100.0	1104	9	HSPAS6	X83493 H.sapiens m
10	435	100.0	1457	6	E35160	E35160 Method for
11	435	100.0	2471	6	I58632	I58632 Sequence 18
12	435	100.0	2471	6	I63530	I63530 Sequence 18
13	435	100.0	2534	6	A87646	A87646 Sequence 4
14	435	100.0	2534	6	ARI63572	ARI63572 Sequence
15	435	100.0	2534	6	ARI73438	ARI73438 Sequence
16	435	100.0	2534	6	E05110	E05110 cDNA encodi
17	435	100.0	2534	6	E09121	E09121 cDNA encodi
18	435	100.0	2534	9	HUMFASANT	M67454 Human Fas a
19	435	100.0	2551	6	ARI43111	ARI43111 Sequence
20	435	100.0	2551	9	HSAP01	X63717 H.sapiens m
21	435	100.0	2719	9	BC012479	BC012479 Homo sapi
22	435	100.0	8282	6	AX146813	AX146813 Sequence
23	435	100.0	8345	6	AX146814	AX146814 Sequence
24	433.4	99.6	1468	6	AX060536	AX060536 Sequence
25	433.4	99.6	1483	6	AX060538	AX060538 Sequence
26	433.4	99.6	3009	6	AX060540	AX060540 Sequence
27	433.4	99.6	3009	6	AX060542	AX060542 Sequence
28	375	86.2	983	9	HSPASAP0A	Z66556 H.sapiens F
29	369.4	84.9	996	9	AB031420	AB031420 Macaca fa
30	366.2	84.2	1342	9	AF344850	AF344850 Macaca ne
31	364.6	83.8	1068	9	AF326208	AF326208 Macaca as
32	363.6	83.6	1005	9	AF332357	AF332357 Macaca ar
33	361.4	83.1	1077	9	AF007572	AF007572 Macaca mu
34	361.4	83.1	1367	9	AF344833	AF344833 Macaca mu
35	359.8	82.7	1361	9	AF344843	AF344843 Cercocebu
36	354	81.4	975	6	AX331556	AX331556 Sequence
37	354	81.4	975	6	AX336715	AX336715 Sequence
38	354	81.4	975	9	HSPAS47	X83492 H.sapiens m
39	334.8	77.0	1840	9	HSAPT9	X81342 H.sapiens A
40	334.8	77.0	1846	11	G75384	G75384 csnpnfrsf6
41	334.8	77.0	2774	9	HSPASX9	X82286 H.sapiens F
42	334.8	77.0	187313	9	AL157394	AL157394 Human DNA
43	307.8	70.8	1324	9	AF344835	AF344835 Aotus tri
44	285	65.5	960	4	AB021298	AB021298 Oryctolag
45	285	65.5	963	4	AB021299	AB021299 Oryctolag

ALIGNMENTS

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LOCUS	H.sapiens	FAS Del3 mRNA.				
DEFINITION	247995					
ACCESSION	247995					
VERSION	247995.1	GI:728580				
KEYWORDS	FAS gene.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	1 (bases 1 to 698)					
JOURNAL	Ruberti, G.					
	Direct Submission					
	Submitted (24-JAN-1995)					
	Ruberti G., Cell Biology Institute, C.N.R.,					

Immunology, viale C. Marx 43, Rome, Italy, I-00137  
 2 (bases 1 to 698)  
 Cascino, I., Fiucci, G., Papoff, G. and Ruberti, G.  
 Three functional soluble forms of the human apoptosis-inducing Fas  
 molecule are produced by alternative splicing  
 J. Immunol. 154 (6), 2706-2713 (1995)  
 95181785  
 7533181  
 On Mar 25, 1995 this sequence version replaced gi:695542.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /isolate="GF"  
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 to a new stop codon at the beginning of exon 7."  
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 197..258  
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 259..341  
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 QY 1 AAGAGAGGAGTACAGAAACATGCAGAGACACAGAGGAAAGCAAGGTTCTCAT 60  
 Db 261 AAGAGAGGAGTACAGAAACATGCAGAGACACAGAGGAAAGCAAGGTTCTCAT 320  
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 Db 321 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATATAATTTATCTGATGTTGACTTGAGT 380

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTAAAGGCTTTGTTTGA 180  
 Db 381 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTAAAGGCTTTGTTTGA 440  
 QY 181 AAGAAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCCAAGACACA 240  
 Db 441 AAGAAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCCAAGACACA 500  
 QY 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTTTCATGGAAGAAAGAGCG 300  
 Db 501 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCACTTTCATGGAAGAAAGAGCG 560  
 QY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCGACAGAAAAATT 360  
 Db 561 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCGACAGAAAAATT 620  
 QY 361 CAGACTATCATCTCCAAAGGACATTACTAGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 420  
 Db 621 CAGACTATCATCTCCAAAGGACATTACTAGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 680  
 QY 421 ATCCAAAGCTTGGTC 435  
 Db 681 ATCCAAAGCTTGGTC 695  
 RESULT 2  
 HSFASCD52  
 LOCUS  
 DEFINITION H.sapiens FAS Del 2 mRNA.  
 ACCESSION 247994  
 VERSION 247994.1 GI:728579  
 KEYWORDS FAS gene.  
 SOURCE Homo sapiens.  
 ORGANISM  
 REFERENCE  
 1 (bases 1 to 761)  
 Ruberti, G.  
 Direct Submission  
 Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,  
 Immunology, viale C. Marx 43, Rome, Italy, I-00137  
 REFERENCE  
 2 (bases 1 to 761)  
 Cascino, I., Fiucci, G., Papoff, G. and Ruberti, G.  
 Three functional soluble forms of the human apoptosis-inducing Fas  
 molecule are produced by alternative splicing  
 J. Immunol. 154 (6), 2706-2713 (1995)  
 95181785  
 7533181  
 On Mar 25, 1995 this sequence version replaced gi:695540.  
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259..321
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322..404
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/number=9
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Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAACATGCGAAGAGCACAGAAAGGAAACCAAGGTTCTCAT 60
DB 324 AAGAGAAAGGAAGTACAGAAACATGCGAAGAGCACAGAAAGGAAACCAAGGTTCTCAT 383
QY 61 GAATCTCCAACTTAAATCCTGGAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120
DB 384 GAATCTCCAACTTAAATCCTGGAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 443
QY 121 AAATATATCAGCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180
DB 444 AAATATATCAGCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 503
QY 181 AAGATGTGTCAATGAAGCCAAATAGATGAGTCAAGATGACAATGCAAGTTCACAGACACA 240
DB 504 AAGATGTGTCAATGAAGCCAAATAGATGAGTCAAGATGACAATGCAAGTTCACAGACACA 563
QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATGGCATCAACTTTCATGGAAGAAAGAACGCG 300
DB 564 GCAGAACAGAAAGTTCAACTGCTGTAATGGCATCAACTTTCATGGAAGAAAGAACGCG 623
QY 301 TATGACACATTTAAAGATCTCAAAAAGCCATCTTTGTACTCTTGCAGAGAAATTT 360
DB 624 TATGACACATTTAAAGATCTCAAAAAGCCATCTTTGTACTCTTGCAGAGAAATTT 683
QY 361 CAGACTATCATCCTCAAGACATTTACTAGTACTCAGAAAAATTCAGAAATTCAGAAATGAA 420
DB 684 CAGACTATCATCCTCAAGACATTTACTAGTACTCAGAAAAATTCAGAAATTCAGAAATGAA 743
QY 421 ATCCAAAGCTTGCTC 435
DB 744 ATCCAAAGCTTGCTC 758
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RESULT 3
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LOCUS
DEFINITION
H. sapiens FAS/Apo 1 mRNA for FAS soluble protein (clone FAS
Exo4,6Del).
ACCESSION
270520
VERSION
1 GI:1418815
KEYWORDS
FAS soluble protein; FAS/Apo 1 gene.
SOURCE
Homo sapiens.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 836)
AUTHORS
Papoff,G., Cascino,I., Eramo,A., Starace,G., Lynch,D.H. and
Ruberti,G.
TITLE
A N-terminal domain shared by Fas soluble variants prevents cell
death in vivo
J. Immunol. (1996) In press
REFERENCE
2 (bases 1 to 846)
AUTHORS
Ruberti,G.
TITLE
Direct Submission
JOURNAL
Immunology, viale C.Marx 43, Rome, Italy, I-00137
FEATURES
Location/Qualifiers
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codon at 397."
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BASE COUNT
ORIGIN
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QY 1 AAGAGAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 60  
 DB 399 AAGAGAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 458  
 QY 61 GAATCTCAACCTTAAATCTGGAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 120  
 DB 459 GAATCTCAACCTTAAATCTGGAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 518  
 QY 121 AAATATATATCACCCTATTTGCTGAGTATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 180  
 DB 519 AAATATATATCACCCTATTTGCTGAGTATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 578  
 QY 181 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 240  
 DB 579 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 638  
 QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
 DB 639 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 698  
 QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAAATT 360  
 DB 699 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAAATT 758  
 QY 361 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 420  
 DB 759 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 818  
 QY 421 ATCCAAAGCTTGGTC 435  
 DB 819 ATCCAAAGCTTGGTC 833

RESULT 4  
 HSFAS346 857 bp mRNA linear PRI 28-NOV-1995  
 LOCUS H.sapiens mRNA for Fas/Apo-1 (clone pCRTM1-Fasdelta(3,4,6)).  
 DEFINITION X83491  
 VERSION X83491.1 GI:971455  
 KEYWORDS FAS gene.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Liu, C., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C., Barr, P.J., and Mountz, J.D.  
 TITLE Protection from Fas-mediated apoptosis by a soluble form of the Fas molecule

JOURNAL Science 263 (5154), 1759-1762 (1999)  
 MEDLINE 94182136  
 PUBMED 7510905

REFERENCE  
 AUTHORS Cheng, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. & Rheum., UAB Station, LHRB 473, Birmingham AL 35294-0007, USA

REFERENCE  
 AUTHORS Liu, C., Cheng, J., and Mountz, J.D.  
 TITLE Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation  
 JOURNAL Biochem. J. 310 (Pt 3), 957-963 (1995)  
 MEDLINE 96013198  
 PUBMED 7575433

COMMENT Related sequences: M67454 and X63717.  
 FEATURES Location/Qualifiers  
 1..857 /organism="Homo sapiens"

gene  
 exon  
 exon

BASE COUNT 302 a 167 c 172 g 216 t  
 ORIGIN

Query Match 100.0%; Score 435; DB 9; Length 857;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-89;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 60  
 DB 286 AAGAGAAGGAGTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCAT 345  
 QY 61 GAATCTCAACCTTAAATCTGGAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 120  
 DB 346 GAATCTCAACCTTAAATCTGGAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 405  
 QY 121 AAATATATATCACCCTATTTGCTGAGTATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 180  
 DB 406 AAATATATATCACCCTATTTGCTGAGTATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGA 465  
 QY 181 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 240  
 DB 466 AAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCCCAAGACACA 525  
 QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
 DB 526 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 585  
 QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAAATT 360  
 DB 586 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTGCAGAGAAAATT 645  
 QY 361 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 420  
 DB 646 CAGACTATCTCTCAAGGACATTTACTAGTACTGACATCGAATAATTCAAACTTCAGAAATGAA 705  
 QY 421 ATCCAAAGCTTGGTC 435  
 DB 706 ATCCAAAGCTTGGTC 720

RESULT 5  
 HSFAS4DEL 899 bp mRNA linear PRI 30-JUN-1996  
 LOCUS H.sapiens Fas/Apo 1 mRNA for Fas soluble protein (clone FAS Exo4Del).  
 DEFINITION 270519  
 VERSION 270519.1 GI:1418817  
 KEYWORDS FAS soluble protein; Fas/Apo 1 gene.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 TITLE 1 (bases 1 to 899)  
 AUTHORS Papoff, G., Cascino, I., Eramo, A., Starace, G., Lynch, D.H., and Ruberfi, G.

REFERENCE  
 TITLE A N-terminal domain shared by Fas soluble variants prevents cell death in vitro  
 JOURNAL J. Immunol. (1996), In press  
 REFERENCE 2 (bases 1 to 899)

AUTHORS Ruberti G.  
TITLE Direct Submission  
JOURNAL Submitted (01-APR-1996) Ruberti G., Cell Biology Institute, C.N.R., Immunology, viale C.Marx 43, Rome, Italy, I-00137

FEATURES  
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197..334  
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335..396  
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/number=5  
/evidence=experimental  
397..459  
/note="Translated in a different frame in this variant up to a new stop codon at 448."  
/number=6  
/evidence=experimental  
460..542  
/number=7  
/note="Not translated in this variant."  
/evidence=experimental  
543..567  
/number=8  
/note="Not translated in this variant."  
/evidence=experimental  
568..>899  
/number=9  
/note="Not translated in this variant."  
/evidence=experimental  
307 a 179 c 197 g 216 t

BASE COUNT 307 a 179 c 197 g 216 t  
ORIGIN  
Query Match 100.0%; Score 435; DB 9; Length 899;  
Best Local Similarity 100.0%; Pred. No. 9.7e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGACAGAAAGGAAACCAAGGTTCTCAT 60  
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Db 462 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGACAGAAAGGAAACCAAGGTTCTCAT 521  
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QY 61 GAATCTCCACCTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120  
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Db 522 GAATCTCCACCTTAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 581  
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QY 121 AAATATATACCACTATTCGTGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 180  
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Db 582 AAATATATACCACTATTCGTGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 641  
QY 181 AAGAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTTCAAGACACA 240  
|||||  
Db 642 AAGAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTTCAAGACACA 701  
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QY 241 GCAGAACAGAAAGTCAACTGCTTCTGTAATTTGGCATCACTTCATCGAAGAAAGCG 300  
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Db 702 GCAGAACAGAAAGTCAACTGCTTCTGTAATTTGGCATCACTTCATCGAAGAAAGCG 761  
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QY 301 TATGACACATTCATTAAAGATCTCAAAAAGCCAAATCTTTGTAATCTTCAGAGAAAT 360  
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Db 762 TATGACACATTCATTAAAGATCTCAAAAAGCCAAATCTTTGTAATCTTCAGAGAAAT 821  
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QY 361 CAGACATCATCTCTCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 420  
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Db 822 CAGACATCATCTCTCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 881  
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QY 421 ATCCAAAGCTTGTC 435  
Db 882 ATCCAAAGCTTGTC 896  
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RESULT 6  
HSFAS34  
LOCUS H.sapiens mRNA for Fas/Apo-1 (clone pCMTM1-Fasdelta(3,4)).  
DEFINITION X83490  
ACCESSION X83490.1 GI:971454  
VERSION X83490.1  
KEYWORDS FAS gene.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 920)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Cheng, J., Zhou, T., Liu, C., Shapiro, J.P., Brauer, M.J., Kiefer, M.C., Bart, P.J. and Mountz, J.D.  
Protection from Fas-mediated apoptosis by a soluble form of the Fas molecule  
Science 263 (5154), 1759-1762 (1994)  
94182136  
PUBMED 7510905  
REFERENCE 2 (bases 1 to 920)  
AUTHORS Cheng, J.  
TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at Birmingham, Division of Clinical Immunol. & Rheum., UAB Station, LHRB 473, Birmingham AL 35294-0007, USA  
3 (bases 1 to 920)  
Liu, C., Cheng, J. and Mountz, J.D.  
Differential expression of human Fas mRNA species upon peripheral blood mononuclear cell activation.  
Biochem. J. 310 (Pt 3), 957-963 (1995)  
96013198  
PUBMED 7575433  
COMMENT Related sequences: M67454 and X63717.  
FEATURES  
Location/Qualifiers  
1..920  
/organism="Homo sapiens"  
/isolate="healthy individual"  
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/chromosome="10"  
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/clone="pCR TM 11-Fas delta(3,4)"  
/cell\_type="peripheral blood mononuclear cells"  
391..637  
/gene="Fas/Apo-1"  
391..637  
/gene="Fas/Apo-1"  
/note="3 and 4"  
312 a 180 c 186 g 242 t

BASE COUNT 312 a 180 c 186 g 242 t  
ORIGIN

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Query Match 100.0%; Score 435; DB 9; Length 920;
Best Local Similarity 100.0%; Pred. No. 9.6e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGTCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60
DB 349 AAGAGAAAGGAGTACAGAAACATGTCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 408
QY 61 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 120
DB 409 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 468
QY 121 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
DB 469 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 528
QY 181 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 529 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 588
QY 241 GCAGAACAGAAAGTTCAACTGCTTAAATGGCATCAACTTCAATGGCAAGAAAGAGCG 300
DB 589 GCAGAACAGAAAGTTCAACTGCTTAAATGGCATCAACTTCAATGGCAAGAAAGAGCG 648
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 360
DB 649 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 708
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTACTGATGATGATGATGATGATGATGATGATGAT 420
DB 709 CAGACTATCATCTCAAGGACATTTACTAGTACTGATGATGATGATGATGATGATGATGATGAT 768
QY 421 ATCCAAAGCTTGCTC 435
DB 769 ATCCAAAGCTTGCTC 783

RESULT 7
HSPASCDL1
LOCUS HSPASCDL1 945 bp mRNA linear PRI 15-DEC-1997
DEFINITION H.sapiens FASTM Del mRNA.
ACCESSION 247993
VERSION 247993.1 GI:728578
KEYWORDS FAS gene.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ruberti, G.
Direct Submission
Submitted (24-JAN-1995) Ruberti G., Cell Biology Institute, C.N.R.,
Immunology, viale C. Merz 43, Rome, Italy, I-00137
Three functional soluble forms of the human apoptosis-inducing Fas
molecule are produced by alternative splicing
J. Immunol. 154 (6), 2706-2711 (1995)
95181785
On Mar 25, 1995 this sequence version replaced gi:695538.
Location/Qualifiers
1..945
/organism="Homo sapiens"
/isolate="GF"
/db_xref="taxon:9606"
/chromosome="10"
/clone="FASTM Del"
/cell_type="PHA-activated PBMC"
1..945
/standard_name="FAS/Apo 1"
/note="Alternative splicing variant of FAS gene missing
exon 6"

CDS
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/evidence-experimental
/product="FAS soluble protein"
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/db_xref="GI:695539"
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RCRLDEGHGLEVEJNCTONTKCRCKPNFNCSTVCEHCDCPCCKEHCIIKECTLT
SNYCKEEVKREVKTKCRKHKRKGSHESPTLAPETVAINLSDVLSKYITTTAGV
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/number=8
/evidence-experimental
614..945
/standard_name="FAS/Apo 1"
/number=9
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333 a 192 c 203 g 217 t
BASE COUNT
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.6e-89;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGAGAAAGGAGTACAGAAACATGTCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60
DB 508 AAGAGAAAGGAGTACAGAAACATGTCAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 567
QY 61 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 120
DB 568 GAATCTCCAACTTAAATCCTGAACAGTGGCAATAAATTTATCTGATCTTGACTTGACT 627
QY 121 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 180
DB 628 AATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 587
QY 181 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 240
DB 688 AAGATGGTGTCAATGAAGCCAAATATAGATGATGATGATGATGATGATGATGATGATGAT 747
QY 241 GCAGAACAGAAAGTTCAACTGCTTAAATGGCATCAACTTCAATGGCAAGAAAGAGCG 300
DB 748 GCAGAACAGAAAGTTCAACTGCTTAAATGGCATCAACTTCAATGGCAAGAAAGAGCG 807
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 360
DB 769 TATGACACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 827
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Db 808 TATGACACATTGATTAAAGATCTCAAAAGGACCAATCTTTGTACTCTTCAGAGAAATTT 867  
QY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 420  
Db 868 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 927  
QY 421 ATCCAAAGCTTGCTC 435  
Db 928 ATCCAAAGCTTGCTC 942

## RESULT 8

E05336  
LOCUS E05336 1008 bp RNA linear PAT 29-SEP-1997  
DEFINITION DNA encoding human Fas protein.  
ACCESSION E05336  
VERSION E05336.1 GI:2173525  
KEYWORDS JP 1993219959-A/2.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1008)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Osada,J.  
TITLE NEW DNA AND PROTEIN CODES THEREWITH  
JOURNAL Patent: JP 1993219959-A/2 31-AUG-1993;

COMMENT OSADA BIO SCI-KENKYUSHO  
OS Homo sapiens (human)  
PN JP 1993219959-A/2  
PD 31-AUG-1993

PI 12-FEB-1992 JP 9992028090  
PC OSADA JUICHI

CC C12N15/12,C07K13/00,C12P21/02;  
CC strandedness: Double;  
CC topology: Linear;

CC \*source: cell\_line=KT-3;  
FH Key Location/Qualifiers

FT CDS 1..1008  
FT /product="Fas protein".

FEATURES  
source  
1..1008  
Location/Qualifiers  
/organism="Homo sapiens"

BASE COUNT 343 a 205 c 217 g 243 t

ORIGIN  
Query Match 100.0%; Score 435; DB 6; Length 1008;  
Best Local Similarity 100.0%; Pred. No. 9.6e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGGTTCTCAT 60  
Db 571 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGGTTCTCAT 630  
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTTGAGT 120  
Db 631 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTTGAGT 690  
QY 121 AAATATATCACCACATTTCTGGAGTCATGACACTAAGTCAAGTTAAAGCCTTTGTTTCA 180  
Db 691 AAATATATCACCACATTTCTGGAGTCATGACACTAAGTCAAGTTAAAGCCTTTGTTTCA 750  
QY 181 AAGATGGTGTCAATGAAGCCAAAATAGATGACAAATGACAAATGACAAATGACAAACACAC 240  
Db 751 AAGATGGTGTCAATGAAGCCAAAATAGATGACAAATGACAAATGACAAATGACAAACACAC 810  
QY 241 GCAGAACAGAAAGTTCAACTGCTTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAACGC 300  
Db 811 GCAGAACAGAAAGTTCAACTGCTTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAACGC 870  
QY 301 TATGACACATTGATTAAAGATCTCAAAAGGACCAATCTTTGTACTCTTCAGAGAAATTT 360

Db 871 TATGACACATTGATTAAAGATCTCAAAAGGACCAATCTTTGTACTCTTCAGAGAAATTT 930  
QY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 420  
Db 931 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTTCAAACTTCAGAAATGAA 990  
QY 421 ATCCAAAGCTTGCTC 435  
Db 991 ATCCAAAGCTTGCTC 1005

## RESULT 9

HSPAS6  
LOCUS HSPAS6 1104 bp mRNA linear PRI 28-NOV-1995  
DEFINITION H.sapiens mRNA for Fas/Apo-1 (clone pCMTM11-FasdeltaTM).  
ACCESSION X83493  
VERSION X83493.1 GI:971457  
KEYWORDS Fas gene.  
SOURCE Homo sapiens.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1104)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Cheng,J., Zhou,T., Liu,C., Shapiro,J.P., Brauer,M.J., Kiefer,M.C.,  
Bart,P.J. and Mountz,J.D.

TITLE Protection from Fas-mediated apoptosis by a soluble form of the Fas  
molecule

JOURNAL Science 263 (5154), 1759-1762 (1994)  
MEDLINE 94182136  
PUBMED 7510905

REFERENCE 2 (bases 1 to 1104)  
Cheng,J.

TITLE Direct Submission  
JOURNAL Submitted (14-DEC-1994) J. Cheng, University of Alabama at  
Birmingham, Division of Clinical Immunol. & Rheum., UAB Station,  
LHRB 473; Birmingham AL 35294-0007, USA

REFERENCE 3 (bases 1 to 1104)  
Liu,C., Cheng,J. and Mountz,J.D.

TITLE Differential expression of human Fas mRNA species upon peripheral  
blood mononuclear cell activation

JOURNAL Biochem. J. 310 (Pt 3), 957-963 (1995)  
MEDLINE 96013198  
PUBMED 7575433

COMMENT Related sequences: M67454 and X63717.  
FEATURES  
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/isolate="healthy individual"  
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/chromosome="10"  
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/clone="PCR TM.11-Fas delta TM"  
/cell\_type="peripheral blood mononuclear cells"

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700..762  
/gene="Fas/Apo-1"

exon  
700..762  
/gene="Fas/Apo-1"  
/number=6

BASE COUNT 384 a 218 c 233 g 269 t

ORIGIN  
Query Match 100.0%; Score 435; DB 9; Length 1104;  
Best Local Similarity 100.0%; Pred. No. 9.5e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGGTTCTCAT 60  
Db 533 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAACCAAGGTTCTCAT 592  
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTTGAGT 120  
Db 593 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTTGAGT 652

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 180  
 Db 653 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 712  
 QY 181 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 240  
 Db 713 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 772  
 QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG 300  
 Db 773 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG 832  
 QY 301 TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTTGTCAGAGAAAATT 360  
 Db 833 TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTTGTCAGAGAAAATT 892  
 QY 361 CAGACTATATCCTCAAGGACATTACTAGTACTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420  
 Db 893 CAGACTATATCCTCAAGGACATTACTAGTACTGACTCAGAAAATTTCAAACTTCAGAAATGAA 952  
 QY 421 ATCCAAAGCTTGGTC 435  
 Db 953 ATCCAAAGCTTGGTC 967

RESULT 10  
 E35160  
 LOCUS E35160 1457 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Method for inducing apoptosis.  
 ACCESSION E35160  
 VERSION E35160.1 GI:18624419  
 KEYWORDS JP 2000102389-A/7.  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 1457)  
 AUTHORS Hagiwara, H., Aotsuka, Y. and Miyahara, J.  
 TITLE Method for inducing apoptosis  
 JOURNAL Patent: JP 2000102389-A 7 11-APR-2000;  
 YOSHIRI HIDE HAGIWARA, HIDEAKI HAGIWARA  
 COMMENT OS Artificial Sequence  
 PN JP 2000102389-A/7  
 PD 11-APR-2000  
 PE 29-SEP-1998 JP 1998291441  
 PR HIDEAKI HAGIWARA, YASUYUKI AOTSUKA, JUNICHI MIYAHARA PC  
 C12N15/09,A61K31/00,A61K48/00,C07K16/42,C07K19/00,C12N5/10, PC  
 C12N15/02//  
 PC (C12N5/10,C12R1:91),C12N15/00,C12N5/00,C12N15/00,(C12N5/00, PC  
 C12R1:91)  
 CC  
 FH Key Location/Qualifiers  
 FT CDS (7)...(1317).  
 FEATURES source  
 1..1457 Location/Qualifiers  
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 /organism="unidentified"  
 BASE COUNT 441 a 309 c 340 g 367 t  
 ORIGIN

Query Match . 100.0%; Score 435; DB 6; Length 1457;  
 Best Local Similarity 100.0%; Pred. No. 9.3e-89;  
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 QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAAGGAAACCAAGGTTCTCAT 60  
 Db 880 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAAGGAAACCAAGGTTCTCAT 939  
 QY 61 GAATCTCCAACTTAAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120  
 Db 940 GAATCTCCAACTTAAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 999  
 QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 180

Db 1000 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 1059  
 QY 181 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 240  
 Db 1060 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 1119  
 QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG 300  
 Db 1120 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG 1179  
 QY 301 TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTTGTCAGAGAAAATT 360  
 Db 1180 TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTTGTCAGAGAAAATT 1239  
 QY 361 CAGACTATATCCTCAAGGACATTACTAGTACTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420  
 Db 1240 CAGACTATATCCTCAAGGACATTACTAGTACTGACTCAGAAAATTTCAAACTTCAGAAATGAA 1299  
 QY 421 ATCCAAAGCTTGGTC 435  
 Db 1300 ATCCAAAGCTTGGTC 1314

RESULT 11  
 I58632  
 LOCUS I58632 2471 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 18 from patent US 5652210.  
 ACCESSION I58632  
 VERSION I58632.1 GI:2477870  
 KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 2471)  
 AUTHORS Barr, P.J., Shapiro, J.P. and Klefer, M.C.  
 TITLE Soluble splice variant of the Fas (APO-1) antigen, Fas.DELTA.TM  
 JOURNAL Patent: US 5652210-A 18 29-JUL-1997;  
 FEATURES Location/Qualifiers  
 1..2471  
 source /organism="unknown"  
 BASE COUNT 807 a 474 c 489 g 701 t  
 ORIGIN

Query Match 100.0%; Score 435; DB 6; Length 2471;  
 Best Local Similarity 100.0%; Pred. No. 9e-89;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAAGGAAACCAAGGTTCTCAT 60  
 Db 702 AAGAGAAAGGAGTACAGAAAACATGCGAAGACACAGAAAAGGAAACCAAGGTTCTCAT 761  
 QY 61 GAATCTCCAACTTAAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120  
 Db 762 GAATCTCCAACTTAAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 821  
 QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 180  
 Db 822 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTTCA 881  
 QY 181 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 240  
 Db 882 AAGATGCTGTCATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGACACA 941  
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 Db 942 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCG 1001  
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 Db 1002 TATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTTGTCAGAGAAAATT 1061  
 QY 361 CAGACTATATCCTCAAGGACATTACTAGTACTGACTCAGAAAATTTCAAACTTCAGAAATGAA 420

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Db 1062 CAGACTATCATCTCTCAGGACATTACTAGTACTCAGAAATTCACAACTTCAGAAATGAA 1121  
QY 421 ATCCAAAGCTTGGTC 435  
Db 1122 ATCCAAAGCTTGGTC 1136  
RESULT 12  
LOCUS I63530 2471 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 18 from patent US 5663070.  
ACCESSION I63530  
VERSION I63530.1 GI:2481103  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2471)  
AUTHORS Barr, P.J., Shapiro, J.P. and Kiefer, M.C.  
TITLE Recombinant production of a soluble splice variant of the Fas (Apo-1) antigen, Fas TM  
JOURNAL Patent: US 5663070-A 18 02-SEP-1997  
FEATURES  
Location/Qualifiers  
source 1..2471  
BASE COUNT 807 a 474 c 489 g 701 t  
ORIGIN  
Query Match 100.0%; Score 435; DB 6; Length 2471;  
Best Local Similarity 100.0%; Pred. No. 9e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 60  
Db 702 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 761  
QY 61 GAATCTCCACCTTAATCTGAGCAGTGGCAATTAATTTATCTGATGTGACTTGAGT 120  
Db 762 GAATCTCCACCTTAATCTGAGCAGTGGCAATTAATTTATCTGATGTGACTTGAGT 821  
QY 121 AAATATATCACCACCTATTGCTGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 180  
Db 822 AAATATATCACCACCTATTGCTGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 881  
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 240  
Db 882 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 941  
QY 241 GCAGAACAGAAAGTTCACCTGAGTCAAGTCTTAAAGGCTTTGTTGCA 300  
Db 942 GCAGAACAGAAAGTTCACCTGAGTCAAGTCTTAAAGGCTTTGTTGCA 1001  
QY 301 TATGACACATTTGATTAAGATCTCAAAAGCCAAATCTTGTACTCTTGCAGAGAAATTT 360  
Db 1002 TATGACACATTTGATTAAGATCTCAAAAGCCAAATCTTGTACTCTTGCAGAGAAATTT 1061  
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 420  
Db 1062 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 1121  
QY 421 ATCCAAAGCTTGGTC 435  
Db 1122 ATCCAAAGCTTGGTC 1136  
RESULT 13  
LOCUS A87646 2534 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 4 from Patent WO9835692.  
ACCESSION A87646  
VERSION A87646.1 GI:6736281  
KEYWORDS

unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2534)  
AUTHORS Scream, G.R. and Xu, X.  
TITLE MATERIALS AND METHODS RELATING TO THE PROTECTION OF USEFUL IMMUNE CELLS  
JOURNAL Patent: WO 9835692-A 4 20-MUG-1998;  
SCREATOR GAVIN ROBERT (GB); ISIS INNOVATION (GB)  
FEATURES  
Location/Qualifiers  
source 1..2534  
/organism="unidentified"  
/db\_xref="taxon:32644"  
BASE COUNT 817 a 487 c 503 g 727 t  
ORIGIN  
Query Match 100.0%; Score 435; DB 6; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 9e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 60  
Db 765 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 824  
QY 61 GAATCTCCACCTTAATCTGAGCAGTGGCAATTAATTTATCTGATGTGACTTGAGT 120  
Db 825 GAATCTCCACCTTAATCTGAGCAGTGGCAATTAATTTATCTGATGTGACTTGAGT 884  
QY 121 AAATATATCACCACCTATTGCTGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 180  
Db 885 AAATATATCACCACCTATTGCTGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGCA 944  
QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 240  
Db 945 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAGACACA 1004  
QY 241 GCAGAACAGAAAGTTCACCTGAGTCAAGTCTTAAAGGCTTTGTTGCA 300  
Db 1005 GCAGAACAGAAAGTTCACCTGAGTCAAGTCTTAAAGGCTTTGTTGCA 1064  
QY 301 TATGACACATTTGATTAAGATCTCAAAAGCCAAATCTTGTACTCTTGCAGAGAAATTT 360  
Db 1065 TATGACACATTTGATTAAGATCTCAAAAGCCAAATCTTGTACTCTTGCAGAGAAATTT 1124  
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 420  
Db 1125 CAGACTATCATCTCTCAAGGACATTTACTAGTACTCAGAAATTTCAAACCTTCAGAAATGAA 1184  
QY 421 ATCCAAAGCTTGGTC 435  
Db 1185 ATCCAAAGCTTGGTC 1199  
RESULT 14  
LOCUS AR163572 2534 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 1 from patent US 6270998.  
ACCESSION AR163572  
VERSION AR163572.1 GI:16234218  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2534)  
AUTHORS Nagata, S., Itoh, N. and Yonehara, S.  
TITLE DNA coding for human cell surface antigen  
JOURNAL Patent: US 6270998-A 1 07-AUG-2001;  
FEATURES  
Location/Qualifiers  
source 1..2534  
/organism="unknown"  
BASE COUNT 817 a 487 c 503 g 727 t  
ORIGIN

Query Match 100.0%; Score 435; DB 6; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 9e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGAGAAAGAAACCAAGGTTCTCAT 60  
DB 765 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGAGAAAGAAACCAAGGTTCTCAT 824

QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATCTTGCATTTGACT 120  
DB 825 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATCTTGCATTTGACT 884

QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 180  
DB 885 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 944

QY 181 AAGATGTTGTCATTAAGCCAAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 945 AAGATGTTGTCATTAAGCCAAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 1004

QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATGGCATCAACTTCTGTAATGGCATCAACTTCTG 300  
DB 1005 GCAGAACAGAAAGTTCAACTGCTTCTGTAATGGCATCAACTTCTGTAATGGCATCAACTTCTG 1064

QY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAATTT 360  
DB 1065 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAAATTT 1124

QY 361 CAGACTATCATCTCCTCAAGGACATTTACTAGTGTACTCAGAAAAATTTCAAACTTTCAAGAAATGAA 420  
DB 1125 CAGACTATCATCTCCTCAAGGACATTTACTAGTGTACTCAGAAAAATTTCAAACTTTCAAGAAATGAA 1184

QY 421 ATCCAAAGCTTGGTC 435  
DB 1185 ATCCAAAGCTTGGTC 1199

Search completed: June 15, 2003, 20:47:49  
Job time : 1284 secs

RESULT 15  
AR173438  
LOCUS AR173438 2534 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 16 from patent US 6306395.  
ACCESSION AR173438  
VERSION AR173438.1 GI:17913758  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2534)  
AUTHORS Nakamura, N. and Nagata, S.  
TITLE Fas antigen derivatives  
JOURNAL Patent: US 6306395-A 16 23-OCT-2001;  
FEATURES  
Location/Qualifiers  
1..2534  
source /organism="unknown"  
BASE COUNT 817 a 487 c 503 g 727 t  
ORIGIN

Query Match 100.0%; Score 435; DB 6; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 9e-89;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGAGAAAGAAACCAAGGTTCTCAT 60  
DB 765 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCAGAGAAAGAAACCAAGGTTCTCAT 824

QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATCTTGCATTTGACT 120  
DB 825 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATCTTGCATTTGACT 884

QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 180  
DB 885 AAATATATCACCACATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA 944

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 18:18:33 ; Search time: 217 Seconds  
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Title: US-09-884-987-1\_COPY\_765\_1199

Perfect score: 435

Sequence: 1 aagagaagaagtagacagaa.....atgaatcccaaggttggtc 435

Scoring table: IDENTITY\_NUC

Gapop 10.0., Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*
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- 12: /SID52/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*
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- 21: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*
- 22: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	100.0	836	24	ABN79685
2	435	100.0	920	17	AA16303
3	435	100.0	920	24	ABK84693
4	435	100.0	1104	17	AA16303
5	435	100.0	1167	17	AA16303
6	435	100.0	1457	21	AAA39167
7	435	100.0	2471	16	AAQ93879
8	435	100.0	2471	20	AAQ24878
9	435	100.0	2534	13	AAQ29959

10	435	100.0	2534	16	AAQ95297
11	435	100.0	2534	17	AA16303
12	435	100.0	2534	18	AAV07002
13	435	100.0	2534	19	AAV32993
14	435	100.0	2551	21	AAV32993
15	435	100.0	2551	24	ABN79588
16	435	100.0	2551	24	ABN79588
17	435	100.0	2551	24	ABN79588
18	435	100.0	2551	24	ABN79588
19	435	100.0	2551	24	ABN79588
20	435	100.0	2551	24	ABN79588
21	435	100.0	2551	24	ABN79588
22	435	100.0	2551	24	ABN79588
23	435	100.0	2551	24	ABN79588
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25	435	100.0	2551	24	ABN79588
26	435	100.0	2551	24	ABN79588
27	435	100.0	2551	24	ABN79588
28	435	100.0	2551	24	ABN79588
29	435	100.0	2551	24	ABN79588
30	435	100.0	2551	24	ABN79588
31	435	100.0	2551	24	ABN79588
32	435	100.0	2551	24	ABN79588
33	435	100.0	2551	24	ABN79588
34	435	100.0	2551	24	ABN79588
35	435	100.0	2551	24	ABN79588
36	435	100.0	2551	24	ABN79588
37	435	100.0	2551	24	ABN79588
38	435	100.0	2551	24	ABN79588
39	435	100.0	2551	24	ABN79588
40	435	100.0	2551	24	ABN79588
41	435	100.0	2551	24	ABN79588
42	435	100.0	2551	24	ABN79588
43	435	100.0	2551	24	ABN79588
44	435	100.0	2551	24	ABN79588
45	435	100.0	2551	24	ABN79588

## ALIGNMENTS

### RESULT 1

ABN79685

ID ABN79685 standard; DNA; 836 bp.

XX ABN79685;

XX ABN79685;

XX 29-JUL-2002 (first entry)

XX Sequence #9 used to generate target oligonucleotides.

DE Human; immunosuppressive; antiinflammatory; hepatotropic;

KW cytostatic; vasotropic; hepatitis; cancer; allograft rejection;

KW ds; Fas.

XX Homo sapiens.

OS Homo sapiens.

XX Key

FT CDS

FT Location/Qualifiers

FT 1..399

FT /tag= a

FT /product= "protein encoded by sequence

FT used create target oligonucleotides"

XX US2002004490-A1.

XX 10-JAN-2002.

XX 09-MAR-2001; 2001US-0802669.

XX 12-APR-1999; 99US-0290640.

XX 18-SEP-2000; 2000US-0665615.

XX (DEAN/) DEAN N M.

XX

PA (MARC/) MARCUSSEON E G.  
PA (WYAT/) WYATT J.  
PA (ZHAN/) ZHANG H.

PI Dean NM, Marcussen EG, Wyatt J, Zhang H;

XX WPI: 2002-204886/26.  
DR P-PSDB: ABP35574.

XX Novel antisense compound targeted to nucleic acid encoding Fas, Fas  
ligand or Fas associated protein-1 is useful for inhibiting expression  
of Fas, Fas ligand, or Fas-1 in cells or tissues, and for treating  
hepatitis

XX Example 18: Page 67-68; 84pp; English.

XX This invention relates to an antisense compound encoding Fas,  
Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition of  
Fas mediated signalling is thought to be immunosuppressive,  
anti-inflammatory, hepatotropic, cytostatic and vasotropic.  
XX Antisense oligonucleotides were designed to target human Fas.  
XX Oligonucleotides were synthesized as chimeric oligonucleotides  
and are useful for treating an animal having an autoimmune or  
inflammatory disease e.g., hepatitis, cancer, a condition associated  
with apoptosis, allograft rejection, or ischemia reperfusion  
injury. Optionally, the above mentioned conditions are prevented by  
contacting the allograft with the antisense oligonucleotide. The  
XX oligonucleotides are used in diagnostics, therapeutics, prophylaxis,  
and as research reagents and in kits. The oligonucleotides are also  
XX useful for research purposes. The present nucleotide sequence is  
XX related to human Fas.

XX Sequence 836 BP; 297 A; 166 C; 183 G; 190 T; 0 other;

Query Match 100.0%; Score 435; DB 24; Length 836;  
Best Local Similarity 100.0%; Pred. No. 1.9e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 399 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 458  
QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGAGTTCAGT 120  
DB 459 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGAGTTCAGT 518  
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 180  
DB 519 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGA 578  
QY 181 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCACAGACACA 240  
DB 579 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATGACAAATGTCACAGACACA 638  
QY 241 GCAGACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTCATGGAAAGAAAGAGCG 300  
DB 639 GCAGACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTCATGGAAAGAAAGAGCG 698  
QY 301 TATGACACATGTTAATGAATCTCAAAAAGCCAACTTTGTTACTCTTTCGAGAGAAAT 360  
DB 699 TATGACACATGTTAATGAATCTCAAAAAGCCAACTTTGTTACTCTTTCGAGAGAAAT 758  
QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGAGTCAAGAAATTCAGAAATGAA 420  
DB 759 CAGACTATCATCTCAAGGACATTAAGTACTGAGTCAAGAAATTCAGAAATGAA 818  
QY 421 ATCCAAAGCTTTGGTC 435  
DB 819 ATCCAAAGCTTTGGTC 833

RESULT 2  
AAT34529

ID

XX

AC

XX

XX

DT

DE

XX

XX

KW

KW

XX

OS

XX

FH

FT

CDS

FT

FT

FT

FT

FT

XX

XX

PN

XX

XX

PD

XX

XX

PF

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XX

PR

XX

XX

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PA

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XX

PI

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DR

XX

XX

XX

PT

PT

XX

XX

PS

XX

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

CC

AAT34529 standard; cDNA: 920 BP.

AAT34529;

10-OCT-1996 (first entry)

Human Fas soluble antigen Fas del3 cDNA.

Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;  
angioimmunoblastic lymphadenopathy; AILD; ss.

Homo sapiens.

Key Location/Qualifiers

26...307

/tag= a

sig\_peptide 26...73

/tag= b

mat\_peptide 74...304

/tag= c

WO9620206-A1.

04-JUL-1996.

22-DEC-1995; 95WO-US17083.

23-DEC-1994; 94US-0371263.

(UABR-) UAB RES FOUND.

Cheng J, Liu C, Mountz JD, Zhou T;

WPI: 1996-321796/32.

P-PSDB; AAR9684.

Natural, soluble form of Fas antigen secreted by human cells is

result of alternative mRNA processing - used to diagnose

Fas-associated disease, e.g. systemic lupus erythematosus

Disclosure: Page 121-122; 152pp; English.

4 Human Fas cDNA variants (AAT34527-30) are derived from alternative

splicing of Fas gene transcripts. They were identified following

PCR amplification of cDNA derived from the peripheral blood

mononuclear cells of systemic lupus erythematosus (SLE) and

angioimmunoblastic lymphadenopathy (AILD) patients and from healthy

subjects. In comparison to the Fas gene (AAT34526), variant Fas del3

(AAT34529) has a deletion of nucleotides 391-637. This deletion causes

frame shifting and an altered amino acid sequence (AAR99683).

Sequence 920 BP; 312 A; 180 C; 186 G; 242 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 920;

Best Local Similarity 100.0%; Pred. No. 1.9e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60

DB 349 AAGAGAAAGGAAGTACAGAAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 408

QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGAGTTCAGT 120

DB 409 GAATCTCCACCTTAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGAGTTCAGT 468

QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTCAGGCTTTGTCGA 180

DB 469 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTCAGGCTTTGTCGA 528

QY 181 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGTCACAGACACA 240

DB 529 AAGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAATGTCACAGACACA 588



angioimmunoblastic lymphadenopathy; AILD; ss.

Homo sapiens.  
Key Location/Qualifiers  
CDS 26..970  
/tag= a  
sig\_peptide 26..73  
/tag= b  
mat\_peptide 74..967  
/tag= c

W09620206-A1.

04-JUL-1996.

22-DEC-1995; 95WO-US17083.

23-DEC-1994; 94US-0371263.

(UABR-) UAB RES FOUND.

Cheng J, Liu C, Mountz JD, Zhou T;

WPI; 1996-321796/32.

P-PSDB; AAR99682.

Natural, soluble form of Fas antigen secreted by human cells is result of alternative mRNA processing - used to diagnose Fas-associated disease, e.g. systemic lupus erythematosus

Disclosure; Page 112-113; 152pp; English.

4 Human Fas cDNA variants (AAT34527-30) are derived from alternative splicing of Fas gene transcripts. They were identified following PCR amplification of cDNA derived from the peripheral blood mononuclear cells of systemic lupus erythematosus (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients and from healthy subjects. In comparison to the Fas gene (AAT34526), variant Fas dell (AAT34528) lacks nucleotides 700-762 as a result of an exon deletion. The encoded protein (AAR99682) lacks the transmembrane region of insoluble Fas antigen (AAR99681). The cDNA can be used for prodn. of recombinant, soluble dell variant or as a specific probe.

Sequence 1104 BP; 384 A; 218 C; 233 G; 269 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 1104;  
Best Local Similarity 100.0%; Pred. No. 2e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 533 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 592  
QY 61 GAATCTCCAACTTAATCTGCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120  
DB 593 GAATCTCCAACTTAATCTGCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 652  
QY 121 AATATATACCACTATTGCTGGAGTATGACACTAAGTCAAGTTAAAGGTTGTTGCA 180  
DB 653 AATATATACCACTATTGCTGGAGTATGACACTAAGTCAAGTTAAAGGTTGTTGCA 712  
QY 181 AAGATGTGTGTAATGAAGCCAAATAGATGATGATCAAGTCAAGTCCAGACACA 240  
DB 713 AAGATGTGTGTAATGAAGCCAAATAGATGATGATCAAGTCAAGTCCAGACACA 772  
QY 241 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCACTTCATGGAAGAAAGAACGCG 300  
DB 773 GCAGAACAGAAAGTTCAACTGCTGTAATTTGGCATCACTTCATGGAAGAAAGAACGCG 832  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCGACAGAAAT 360  
DB 833 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCGACAGAAAT 892

QY 361 CAGACTATCATCTCTCAAGGACATCTACTAGTCTCAGAAATTTCAAACTTCAGAAATGAA 420  
DB 893 CAGACTATCATCTCTCAAGGACATCTACTAGTCTCAGAAATTTCAAACTTCAGAAATGAA 952  
QY 421 ATCCAAAGCTTGTC 435  
DB 953 ATCCAAAGCTTGTC 967

RESULT 5

AAT34526

ID AAT34526 standard; cDNA; 1167 BP.

XX AAT34526;

DT 10-OCT-1996 (first entry)

XX Human Fas antigen cDNA.

XX Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;  
XX angioimmunoblastic lymphadenopathy; AILD; ss.

OS Homo sapiens.

Key Location/Qualifiers

CDS 26..1033

FT sig\_peptide /tag= a

FT 26..73

FT mat\_peptide /tag= b

FT 74..1030

FT /tag= c

XX W09620206-A1.

PN 04-JUL-1996.

XX 22-DEC-1995; 95WO-US17083.

XX 23-DEC-1994; 94US-0371263.

XX (UABR-) UAB RES FOUND.

XX Cheng J, Liu C, Mountz JD, Zhou T;

XX WPI; 1996-321796/32.

XX P-PSDB; AAR99681.

XX Natural, soluble form of Fas antigen secreted by human cells is

XX result of alternative mRNA processing - used to diagnose

XX Fas-associated disease, e.g. systemic lupus erythematosus

XX Disclosure; Page 107-108; 152pp; English.

XX A cDNA clone (AAT34526) codes for a membrane receptor-like protein,  
XX Fas antigen (AAR99681). It was isolated from cDNA derived from the  
XX peripheral blood mononuclear cells of systemic lupus erythematosus  
XX (SLE) and angioimmunoblastic lymphadenopathy (AILD) patients, and  
XX from healthy subjects, by PCR amplification. In addition to fas  
XX cDNA, 4 other PCR products were obt'd. (see also AAT34527-30). These  
XX coded for soluble forms (AAR99682-85) of Fas antigen that are present  
XX at higher levels in SLE and AILD patients than the non-soluble Fas  
XX antigen.

XX Sequence 1167 BP; 394 A; 231 C; 247 G; 295 T; 0 other;

Query Match 100.0%; Score 435; DB 17; Length 1167;

Best Local Similarity 100.0%; Pred. No. 2e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 596 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 655



QY	61	GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTATATCTGATGTGACTTCAGT	120
Db	656	GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTATCTGATGTGACTTCAGT	715
QY	121	AAATATATCACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGCGTTTGTTCGA	180
Db	716	AAATATATCACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGCGTTTGTTCGA	775
QY	181	AAGAAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGAATGACAATGTCCCAAGACACA	240
Db	776	ARGAAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGAATGACAATGTCCCAAGACACA	835
QY	241	GCAGACAGAAAGTTCAACTGCTTCGTPAATGGCATCAACTTCATGGAAGAAGAAGACGG	300
Db	836	GCAGACAGAAAGTTCAACTGCTTCGTPAATGGCATCAACTTCATGGAAGAAGAAGACGG	895
QY	301	TATGACACATTTGATTTAAAGATCTCAAAAAGCCAACTTTGTACTCTTGACAGAGAAAATT	360
Db	896	TATGACACATTTGATTTAAAGATCTCAAAAAGCCAACTTTGTACTCTTGACAGAGAAAATT	955
QY	361	CAGACTATCATCTCAAGGCACATTACTTAGTGACTCAGAAAATTCAAACCTTCAGAAATGAA	420
Db	956	CAGACTATCATCTCAAGGCACATTACTTAGTGACTCAGAAAATTCAAACCTTCAGAAATGAA	1015
QY	421	ATCCAAAGCTTGGTC	435
Db	1016	ATCCAAAGCTTGGTC	1030

RESULT 6	
AAA39167	
ID	AAA39167 standard; DNA; 1457 BP.
XX	
AC	AAA39167;
XX	
DT	05-SEP-2000 (first entry)
XX	
DE	Apoptobody3sc fusion protein encoding nucleotide sequence SEQ ID NO:7.
XX	
KW	Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
XX	medical; pharmaceutical; pharmacological; biochemical; ds.
OS	Homo sapiens.
OS	Synthetic.

JP2000102389-A.  
11-APR-2000.  
29-SEP-1998; 98JP-0291441.  
29-SEP-1998; 98JP-0291441.  
(HAGI/) HAGIWARA Y.  
(HAGI/) HAGIWARA H.  
WPI: 2000-332086/29.  
P-PSDB; AAY91029.  
Causing apoptosis comprises transfecting fused gene to cell and reacting cell with idiotypic antibody -  
Disclosure; Page 7; 10pp; Japanese.

transfected to a cell to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmaceutical, pharmacological and biochemical fields. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention.

CC transfect to a cell to express the fused gene and then an idiotype antibody is reacted with the expressed cell. The method is useful in medical, pharmaceutical, pharmacological and biochemical fields. The present sequence encodes a fusion protein designated apoptobody3sc, which is used in the exemplification of the present invention.

XX

SQ Sequence 1457-BP; 441 A; 309 C; 340 G; 367 T; 0 other;

Query Match 100.0%; Score 435; DB 21; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 2.2e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGAGAAAGAGTACAGAAAACATCGAGAAACACAGAAAGAGAAACCAAGGTTCTCAT 60  
DB 880 AGAGAGAAAGAGTACAGAAAACATCGAGAAACACAGAAAGAGAAACCAAGGTTCTCAT 939  
QY 61 GAATCTCCAAACCTTAAATCCTCGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120  
DB 940 GAATCTCCAAACCTTAAATCCTCGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 999  
QY 121 AAATATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 180  
DB 1000 AAATATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 1059  
QY 181 AGAANTGGTGTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA 240  
DB 1060 AAGAANTGGTGTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGTCCAAGACACA 1119  
QY 241 GCAGACAGAAAGCTTCAACTGCTTCTGTAATTTGGCATCAACTTCTGTAAGAAAGAAAGCG 300  
DB 1120 GCAGACAGAAAGCTTCAACTGCTTCTGTAATTTGGCATCAACTTCTGTAAGAAAGAAAGCG 1179  
QY 301 TATGACACATTTGATTAAAGATCTCAAAAGGCCAATCTTTGTACTCTTTCAGAGAGAAAT 360  
DB 1180 TATGACACATTTGATTAAAGATCTCAAAAGGCCAATCTTTGTACTCTTTCAGAGAGAAAT 1239  
QY 361 CAGACTATATCTCCTCAAGGACATATCTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA 420  
DB 1240 CAGACTATATCTCCTCAAGGACATATCTAGTGACTCAGAAAATTCAAACTTCAGAAATGAA 1299  
QY 421 ATCCAAAGCTTGCTC 435  
DB 1300 ATCCAAAGCTTGCTC 1314

RESULT 7  
AAQ93879  
ID AAQ93879 standard; cDNA; 2471 BP.  
XX  
XX AAQ93879;  
XX  
DT 06-NOV-1995 (first entry)  
XX  
DE Fas-delta-TM cDNA.  
XX  
XX Fas-delta-TM; transmembrane deletion; apoptosis; antibody;  
KW adoptive immunotherapy; transgenic animal; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Location/Qualifiers  
CDS 195..1139  
FT FT \*tag= a  
FT FT 195..242  
FT FT /\*tag= b  
FT FT 243..1136  
FT FT /\*tag= c  
XX  
XX WO9513701-A.  
XX  
XX 26-MAY-1995.  
XX  
XX 15-NOV-1994. 94WO-US13173.

XX 15-NOV-1993; 93US-0152443.  
XX (LXRB-) LXR BIOTECHNOLOGY INC.  
XX Barr PJ, Kiefer MC, Shapiro JP;  
XX WPI: 1995-200120/26.  
XX P-PSDB; AAR76238.  
XX New nucleic acid encoding Fas protein without its trans-membrane region  
XX - and related vectors, transformed cells, transgenic animals, protein and  
XX antibodies, useful for control of Fas mediated apoptosis  
XX Claim 3; Fig.3-1 to 3-4; 38pp; English.  
XX mRNA was obtd. from human lymphocytes and PCR was used to make  
XX cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane  
XX region) mRNA. The PCR product was ligated into pBluescript and the  
XX recombinant plasmid was used to transfect E. coli DH5-alpha cells. The  
XX insert sequence of pBluescript-Fas-delta-TM is given in AAQ93879.  
XX Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;  
Query Match 100.0%; Score 435; DB 16; Length 2471;  
Best Local Similarity 100.0%; Pred. No. 2.6e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGAAAGAGTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGTTCTCAT 60  
Db 702 AGAGAAAGAGTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGTTCTCAT 761  
QY 61 GAATCTCCAACTTAATCCTGAACAGTGGCAATAAATTTATCTGATGTTGACGTGAGT 120  
Db 762 GAATCTCCAACTTAATCCTGAACAGTGGCAATAAATTTATCTGATGTTGACGTGAGT 821  
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCGA 180  
Db 822 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCGA 881  
QY 181 AGAATGGTGTCAATGAAGCCAAATPAGATGATGATCAAGAATGACAATGCTCAAGACACA 240  
Db 882 AGAATGGTGTCAATGAAGCCAAATPAGATGATGATCAAGAATGACAATGCTCAAGACACA 941  
QY 241 GCAGACACAGAAAGTCAACTGCTTCTGTAATGGCATCACTTCATGGAAGAAAGAGCG 300  
Db 942 GCAGACACAGAAAGTCAACTGCTTCTGTAATGGCATCACTTCATGGAAGAAAGAGCG 1001  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAACTTTGTACTCTTCAGAGAAAT 360  
Db 1002 TATGACACATTTGATTAAGATCTCAAAAAGCCAACTTTGTACTCTTCAGAGAAAT 1061  
QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGACTCAGAAATTCAGAAATTCAGAAATGAA 420  
Db 1062 CAGACTATCATCTCAAGGACATTAAGTACTGACTCAGAAATTCAGAAATTCAGAAATGAA 1121  
QY 421 ATCCAAAGCTTGGTC 435  
Db 1122 ATCCAAAGCTTGGTC 1136  
RESULT 8  
AAX24878  
ID AAX24878 standard; DNA; 2471 BP.  
XX AAX24878;  
XX AC AC  
XX AT AT  
XX TT TT  
XX XX (first entry)  
DE Soluble Fas receptor DNA.  
KW Fas receptor; Fas ligand; FasL; proinflammatory; immunosuppressive;  
KW graft versus host disease; autoimmune disease; psoriasis;

XX rheumatoid arthritis; systemic lupus erythematosus; gene therapy;  
XX ss.  
XX Mammalia.  
XX Key Location/Qualifiers  
XX CDS 195..1139  
XX /tag= a  
XX /transl\_except= (pos:519..521, aa:Gly)  
XX sig\_peptide 195..242  
XX /tag= b  
XX mat\_peptide 243..1136  
XX /tag= c  
XX polyA\_signal 2349..2354  
XX /tag= d  
XX polyA\_signal 2455..2460  
XX /tag= e  
XX WO9903999-A1.  
XX 28-JAN-1999.  
XX 16-JUL-1998; 98WO-US14771.  
XX 17-JUL-1997; 97US-0052829.  
XX (UNMI ) UNIV MICHIGAN.  
XX Chen J, Nabel GJ;  
XX WPI: 1999-132243/11.  
XX P-PSDB; AAW98070.  
XX Inhibition of proinflammatory responses - using an agent which  
XX modulates FasL stimulation, used for treating graft versus host  
XX disease or autoimmune disease  
XX Disclosure; Fig 4B; 71pp; English.  
XX This present sequence is a DNA clone encoding soluble Fas receptor  
XX (see AAW98070). The invention provides a method for inhibiting a  
XX proinflammatory response in a cell mixture by administering an  
XX immunosuppressive agent which inhibits the proinflammatory activity  
XX of Fas ligand (FasL). In some embodiments, FasL is coadministered  
XX with the immunosuppressive agent, and the cell mixture comprises  
XX neutrophil cells. The method can be practised in vitro, ex vivo or  
XX in vivo. Suitable immunosuppressive agents include antisense  
XX molecules that inhibit endogenous FasL expression, soluble Fas  
XX receptors, ribozymes that inhibit the endogenous expression of  
XX FasL, drugs that inhibit FasL signalling, agents that induce the  
XX endogenous expression of transforming growth factor (TGF)-beta,  
XX and polynucleotides coding for an immunosuppressive agent such as  
XX TGF-beta. The method can be used for treating diseases associated  
XX with an undesired FasL-mediated proinflammatory response, e.g.  
XX graft versus host disease, or an autoimmune disease such as  
XX systemic lupus erythematosus, rheumatoid arthritis and psoriasis.  
XX The invention also provides a method for identifying agents which  
XX modulate FasL stimulation of a proinflammatory response.  
XX Sequence 2471 BP; 807 A; 474 C; 489 G; 701 T; 0 other;  
Query Match 100.0%; Score 435; DB 20; Length 2471;  
Best Local Similarity 100.0%; Pred. No. 2.6e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGAGAAAGAGTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGTTCTCAT 60  
Db 702 AGAGAAAGAGTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGTTCTCAT 761  
QY 61 GAATCTCCAACTTAATCCTGAACAGTGGCAATAAATTTATCTGATGTTGACGTGAGT 120  
Db 762 GAATCTCCAACTTAATCCTGAACAGTGGCAATAAATTTATCTGATGTTGACGTGAGT 821

QY 121 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
Db 822 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 881  
QY 181 AGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAAATGTCGAAGACACA 240  
Db 882 AGAATGGTGTCAATGAAGCAAAATAGATGAGATGAGATGACAAATGTCGAAGACACA 941  
QY 241 GCAGACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300  
Db 942 GCAGACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1001  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 360  
Db 1002 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 1061  
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTCAACTTCAGAAATGAA 420  
Db 1062 CAGACTATCATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTCAACTTCAGAAATGAA 1121  
QY 421 ATCCAAAGCTTGTC 435  
Db 1122 ATCCAAAGCTTGTC 1136

RESULT 9

ID AAQ29959 standard; cDNA to mRNA; 2534 BP.

AC AAQ29959;

XX 12-MAR-1993 (first entry)

XX Human cell surface antigen.

XX Fas antigen; apoptosis; pF58; NGFR/TNFR family; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT sig\_peptide 195..242

FT mat\_peptide 243..1199

FT conflict 1046

FT polyA\_signal 1831..1836

FT polyA\_signal 2352..2357

FT polyA\_signal 2518..2523

FT note="this residue is not present in pF3"

FT polyA\_signal 1831..1836

FT polyA\_signal 2352..2357

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

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FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

FT polyA\_signal 2518..2523

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Claim 3; Fig 1 and 2; 27pp; English.

A cDNA library was prepared from polyA+ RNA from the human lymphoma cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-7 cells which were then suspended in buffer containing murine anti-Fas Ab. The cells were "panned" on plates pre-coated with goat anti-mouse antibodies. The Fas-expressing cells adhered to the plates. Extrachromosomal DNA was prepared from adhered cells and used to transform E.coli WMI00 cells. A 520bp XhoI-BamHI fragment from a positive clone (pF3) was used to screen the KT-3 cDNA library. The longest cDNA clone was designated pF58 and contains an ORF corresp. to a 335 amino acid pre-protein and a 319 amino acid mature protein (i.e. human Fas antigen).

Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 13; Length 2534;

Best Local Similarity 100.0%; Pred. No. 2.6e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGAAAGGAGTACAGAAACATCGAAGACGACAGAAAGGAAACCAAGTTCTCAT 60

Db 765 AGAGAAAGGAGTACAGAAACATCGAAGACGACAGAAAGGAAACCAAGTTCTCAT 824

QY 61 GAATCTCCACCTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGT 120

Db 825 GAATCTCCACCTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTCAGT 884

QY 121 AATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180

Db 885 AATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 944

QY 181 AGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCGAAGACACA 240

Db 945 AGAATGGTGTCAATGAAGCCAAATAGATGAGATGAGATGACAAATGTCGAAGACACA 1004

QY 241 GCAGACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300

Db 1005 GCAGACAGAAAGTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1064

QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 360

Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATTTTGTACTCTTGCAGAGAAAT 1124

QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTCAACTTCAGAAATGAA 420

Db 1125 CAGACTATCATCTCTCAAGGACATTTACTAGTGAATTCAGAAATTCAACTTCAGAAATGAA 1184

QY 421 ATCCAAAGCTTGTC 435

Db 1185 ATCCAAAGCTTGTC 1199

RESULT 10

AAQ95297

ID AAQ95297 standard; cDNA; 2534 BP.

XX AAQ95297;

XX 19-FEB-1996 (first entry)

XX Plasmid pF58 contg. human Fas cDNA.

XX Plasmid pF58; human Fas cDNA; soluble membrane protein;

XX antibody production; diseases; treatment; prevention; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 195..1202

XX /\*tag= a

priority

XX Itoh N, Nagata S, Yonehara S;

XX WPI; 1992-358914/44.

XX P-PSDB; AAR28084.

XX DNA encoding human cell surface antigen - used to clarify

XX apoptosis mechanism of various types of cell, and to prepare

XX monoclonal antibodies that react with tumour cells expressing Fas

XX

XX

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XX



Db 945 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAATGTCCAGACACA 1004  
 Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
 Db 1005 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 1064  
 Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 360  
 Db 1065 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 1124  
 Qy 361 CAGACTATCATCCCTCAAGGACATTTAGTGACTCAGAAAAATTTCAAACTTTCAGAAATGAA 420  
 Db 1125 CAGACTATCATCCCTCAAGGACATTTAGTGACTCAGAAAAATTTCAAACTTTCAGAAATGAA 1184  
 Qy 421 ATCCAAAGCTTGGTC 435  
 Db 1185 ATCCAAAGCTTGGTC 1199

## RESULT 12

AAV07002  
 ID AAV07002 standard; cDNA to mRNA; 2534 BP.

XX  
 AC AAV07002;  
 DT 16-JUL-1998 (first entry)  
 XX

DE Human Fas antigen cDNA.

XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;  
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;  
 KW apoptosis modulation; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH 195..1202  
 FT CDS /\*tag= a  
 FT sig\_peptide 195..242  
 FT mat\_peptide 243..1199  
 FT /\*tag= b  
 FT /\*tag= c  
 FT /\*product= Fas\_antigen

XX MO9742319-A1.

XX 13-NOV-1997.

XX 01-MAY-1997; 97WO-JP01502.

XX 02-MAY-1996; 96JP-0135760.

XX (MOCH) MOCHIDA PHARM CO LTD.  
 XX (OSAB-) OSAKA BIOSCIENCE INST.

XX Negata S, Nakamura N;

XX WPI; 1997-558981/51.

XX P-PSDB; AAW50289.

XX Fas antigen derivative containing modified extracellular region -  
 PT has low antigenicity, promotes apoptosis and is useful in treatment  
 PT of viral and other diseases

XX Disclosure; Fig 1-2; 102pp; Japanese.

XX The present sequence was used in the development of novel Fas  
 CC antigen derivatives, which contain a Fas antigen extracellular  
 CC region lacking one or more amino acid residues in the region from  
 CC the amino-terminal to (but excluding) the 1st cysteine residue  
 CC (preferably at least 29 residues are deleted).  
 CC The derivatives are effective regulators of apoptosis and can be  
 CC used (either by administration of the polypeptide, or by the use

CC of the coding DNA in gene therapy) to treat a range of diseases,  
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases  
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of  
 CC virus-infected cells.

XX  
 SQ Sequence 2534 BP; 817 A; 491 C; 499 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 18; Length 2534;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-108;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAAAACCAAGGTTCTCAT 60  
 Db 765 AAGAGAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGGAAAAACCAAGGTTCTCAT 824  
 Qy 61 GAATCTCCAACCTTAAATCTCTGAAACAGAGTGGCAATATTTATCTGATGTTGACTTGGT 120  
 Db 825 GAATCTCCAACCTTAAATCTCTGAAACAGAGTGGCAATATTTATCTGATGTTGACTTGGT 884  
 Qy 121 AATATATATCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTTTGA 180  
 Db 885 AATATATATCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTTTGA 944  
 Qy 181 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACAATGTCCAAGACACA 240  
 Db 945 AAGATGGTGTCAATGAAGCAAAATAGATGAGATGACAATGTCCAAGACACA 1004  
 Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
 Db 1005 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 1064  
 Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 360  
 Db 1065 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTT 1124  
 Qy 361 CAGACTATCATCCCTCAAGGACATTTAGTGACTCAGAAAAATTTCAAACTTTCAGAAATGAA 420  
 Db 1125 CAGACTATCATCCCTCAAGGACATTTAGTGACTCAGAAAAATTTCAAACTTTCAGAAATGAA 1184  
 Qy 421 ATCCAAAGCTTGGTC 435  
 Db 1185 ATCCAAAGCTTGGTC 1199

## RESULT 13

AAV32993  
 ID AAV32993 standard; cDNA; 2534 BP.

XX AC AAV32993;

XX 18-NOV-1998 (first entry)

XX Fas cDNA.

XX Fas protein; CD8+ T-lymphocyte killer cell; TK; Fas-ligand; FasL;  
 KW CD4+ cell; apoptosis; lymphocyte; human immunodeficiency virus; HIV;  
 KW simian immunodeficiency virus; SIV; cytotoxic T lymphocyte; CTL;  
 KW prophylactic; AIDS; ss.

XX Mammalia sp.

XX Key Location/Qualifiers  
 FH 195..1202  
 FT CDS /\*tag= a  
 FT sig\_peptide 195..242  
 FT mat\_peptide 243..1199  
 FT /\*tag= b  
 FT /\*tag= c  
 FT polyA\_signal 1831..1836  
 FT /\*tag= d  
 XX MO9835692-A1.

XX PD 20-AUG-1998.  
XX PF 17-FEB-1998; 98WO-GB00485.  
XX PR 17-FEB-1997; 97GB-0003276.  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PI Sreaton GR, Xu X;  
XX WP1: 1998-456867/39.  
DR P-PSDB; AAW49104.  
XX  
XX Reducing CD8+ lymphocyte apoptosis to treat e.g. immunodeficiency  
XX diseases - by interfering with interaction of Fas with Fas-ligand  
XX expressed on activated CD4+ cells, e.g. cells infected with HIV  
XX  
XX Disclosure; Fig 10; 71pp; English.  
XX  
XX The present sequence represents a Fas cDNA sequence used in the  
XX method of the invention. The method is concerned with reducing  
XX depletion of activated Fas-expressing CD8+ T-lymphocyte killer (TK)  
XX cells in an immune cell population which also comprises of Fas-ligand  
XX (FasL)-expressing activated CD4+ cells. It involves contacting this  
XX immune cell population with an effective amount of an agent (e.g. a  
XX soluble Fas-Fc fusion protein) which would interfere with the  
XX interaction between Fas and FasL. Therefore, the method is useful for  
XX identifying suitable agents which can reduce depletion of activated  
XX Fas-expressing CD8+ TK cells in immune cell populations. Also claimed  
XX is the use of the agent in the manufacture of therapeutic compositions.  
XX Apoptosis of lymphocytes can be triggered by the interaction of the  
XX cell surface receptor Fas and its ligand FasL. By interfering with  
XX this interaction, the method described and its preparations can prevent  
XX apoptosis of CD8+ TK lymphocytes caused by expression of FasL on  
XX activated CD4+ cells. Such FasL-expressing activated CD4+ cells are  
XX especially the result of CD4+ cell infection with an immunodeficiency  
XX virus e.g. human immunodeficiency virus (HIV) or simian immunodeficiency  
XX virus (SIV). The claimed prevention of apoptosis may then allow  
XX maintenance/regeneration of cytotoxic T lymphocyte (CTL) activity  
XX towards the CD4+ cells infected with the infectious agent, enabling  
XX treatment (prophylactic and/or therapeutic) of immunodeficiency  
XX diseases e.g. AIDS.  
XX  
XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

Query Match 100.0%; Score 435; DB 19; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 2.6e-108;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGAAAGGAAGTACAGAAACATCGAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60  
DB 765 AGAGAAAGGAAGTACAGAAACATCGAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 824  
OY 61 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120  
DB 825 GAATCTCCAACTTAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 884  
OY 121 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCGA 180  
DB 885 AATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCGA 944  
OY 181 AGAATGGTGTCAATCAAGCCAAATAGATGAGATCAAGATGACATGATGTCAGACACA 240  
DB 945 AGAATGGTGTCAATCAAGCCAAATAGATGAGATGACATGATGTCAGACACA 1004  
OY 241 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATGAAAGAAAGGCG 300  
DB 1005 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATGAAAGAAAGGCG 1064  
OY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCAGAGAAAT 360  
DB 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCAGAGAAAT 1124

OY 361 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTCAGAAATTCAGAAATGAA 420  
DB 1125 CAGACTATCATCTCTCAAGGACATTACTAGTACTCAGAAATTCAGAAATTCAGAAATGAA 1184  
OY 421 ATCCAAAGCTTGGTC 435  
DB 1185 ATCCAAAGCTTGGTC 1199

## RESULT 14

AAC61798  
ID AAC61798 standard; DNA; 2551 BP.

XX AAC61798;

XX AC  
XX 06-MAR-2001 (first entry)XX DT  
XX DNA encoding a human Fas (Apo-1) protein.

XX KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;  
XX KW Fas associated protein 1; protein tyrosine phosphatase; cancer;  
XX KW autoimmune disease; inflammatory disease; lymphoma; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
XX FT CDS 221..1228  
XX FT /\*tag= a  
XX FT /product= "Fas"

XX PN WO200061150-A1.

XX XX 19-OCT-2000.

XX XX 10-APR-2000; 2000WO-US09540.

XX PR 12-APR-1999; 99US-0290640.

XX XX (ISIS-) ISIS PHARM INC.

XX PA Dean NM, Marcussen EG;

XX PI WPI: 2000-628395/60.

XX DR P-PSDB; AAB19341.

XX Antisense oligonucleotides for treating hepatitis and colon, liver or  
XX lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein  
XX 1 (Fas-1) expression

XX PS Example 2; Page 71-73; 116pp; English.

XX The present sequence encodes human Fas (Apo-1). The specification  
XX describes antisense compounds which are targeted to the 5'-untranslated  
XX region, translational start site, translational termination region  
XX or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas  
XX ligand (FasL), or Fas-1 (Fas associated protein 1, protein tyrosine  
XX phosphatase). The antisense compounds are used to inhibit the  
XX expression of Fas, FasL or Fas-1 in cells or tissues. They are used  
XX to treat autoimmune or inflammatory diseases such as hepatitis. They  
XX can also be used to treat cancer, especially colon, liver or lung  
XX cancer or lymphoma.

XX SQ Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

Query Match 100.0%; Score 435; DB 21; Length 2551;

Best Local Similarity 100.0%; Pred. No. 2.6e-108;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGAGAAAGGAAGTACAGAAACATCGAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 60

DB 791 AGAGAAAGGAAGTACAGAAACATCGAGAAAGCAGAGAAAGAAACCAAGTTCTCAT 850  
|||||  
|||||

61	QY	GAATCTCCAACTTAATAATCCTGAAACAGTGGCAATAAATTTATCTGATGTGACTTGAGT	120
851	Db	GAATCTCCAACTTAATAATCCTGAAACAGTGGCAATAAATTTATCTGATGTGACTTGAGT	910
121	QY	AAATATATCACCACACTATTCTGGAGTCATGCACACTAAGTCAAGTTAAAGGCTTTGTTCGA	180
911	Db	AAATATATCACCACACTATTCTGGAGTCATGCACACTAAGTCAAGTTAAAGGCTTTGTTCGA	970
181	QY	AAGAATGGTGTCAAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	240
971	Db	AAGAATGGTGTCAAATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	1030
241	QY	GCAGAACAGAAAGTTCCAATGCTTCTTAATGTGCATCAACTTCATGGAAAGAAAGCG	300
1031	Db	GCAGAACAGAAAGTTCCAATGCTTCTTAAATGTGCATCAACTTCATGGAAAGAAAGCG	1090
301	QY	TATGACACATTGATTAAGACTCTCAAAAAGCCAACTTTGTACTCTTCGAGAGAAAAT	360
1091	Db	TATGACACATTGATTAAGACTCTCAAAAAGCCAACTTTGTACTCTTCGAGAGAAAAT	1150
361	QY	CAGACTATCATCCTCAAGGACATTTACTAGTGTACTCAGAAAAATTCAAAACCTTCAGAAATGAA	420
1151	Db	CAGACTATCATCCTCAAGGACATTTACTAGTGTACTCAGAAAAATTCAAAACCTTCAGAAATGAA	1210
421	QY	ATCCAAAAGCTTGGTC	435
1211	Db	ATCCAAAAGCTTGGTC	1225

## RESULT 15

RESULT 1:  
ABN79588

ABN/9588  
ID ABN79588 standard; DNA: 2551 bp.

XX  
XX  
DT  
0906 / NBNV

XX  
AC ABN79588:

AC  
XX  
ABN/9588;

29-JUL-2002 / first entr

XX  
2007-700-62 IN JSTT)

Human Fas locus HSAP01.

XX  
DE  
HUMAN FAS TOSUS HENFOT.

Human; immunosuppressive

KW cytostatic; vasotropic;

KW ds; Fas.

XX  
XX

OS Homo sapiens.

XX

FH	Key	Location
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
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91	91	91
92	92	92
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94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	CDS	221..123

FT

FT ... /product

XX  
.....  
:

PN US200200490-A1.

XX  
10-TM-3003

PD 10-JAN-2002.

XX  
DE 00-MAB-2001. 2001WC-000-

PF 09-MAR-2001; 2001US-0801  
YY

XX  
DP 12-APP-1000: 00115-0300

PR 17=APR=1999; 9905=029059

XX  
PJ 0007-DES-8T 990-500007

XX (DEAN/) DEAN N M.

Example 2; Page 25-27; 84pp; English.

This invention relates to an antisense compound encoding Fas, Fas ligand, or Fas associated protein-1 (Fap-1). The inhibition of Fas mediated signalling is thought to be immunosuppressive, antiinflammatory, hepatotropic, cytostatic and vasotropic. Antisense oligonucleotides were designed to target human Fas. Oligonucleotides were synthesised as chimeric oligonucleotides and are useful for treating an animal having an autoimmune or inflammatory disease e.g., hepatitis, cancer, a condition associated with apoptosis, allograft rejection, or ischemia reperfusion injury. Optionally, the above mentioned conditions are prevented by contacting the allograft with the antisense oligonucleotide. The oligonucleotides are used in diagnostics, therapeutics, prophylaxis and as research reagents and in kits. The oligonucleotides are also useful for research purposes. The present nucleotide sequence is related to human Fas.

Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

Query Match	100.0%	Score 435	DB 24	Length 2551
-------------	--------	-----------	-------	-------------

Best Local Similarity

Matches 435; Conservative 0; Mismatches 0;

1	QY	AAGAGAAAGAAAGTACAGAAACATCGAAGACCAGAGAAAGGAAACCAAGTTCCTCAT	60
791	Db	AAGAGAAAGAAAGTACAGAAACATCGAAGACCAGAGAAAGGAAACCAAGTTCCTCAT	850
61	QY	GAATCTCCACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTCATGTGTGACTTGAAGT	120
851	Db	GAATCTCCACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTCATGTGTGACTTGAAGT	910
121	QY	AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCCTTTGTTCCGA	180
911	Db	AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCCTTTGTTCCGA	970
181	QY	AGAATGGTGTCNAATGAAGCCAAATAATAGATGAGATCAAGAATGACAATGTCCCAAGACACA	240
971	Db	AGAATGGTGTCNAATGAAGCCAAATAATAGATGAGATCAAGAATGACAATGTCCCAAGACACA	1030
241	QY	GCAGAACAGAAAGTTCAACTGCTTCTTAATTTGGCATCAACTTCATGGAAGAAGAGCG	300
1031	Db	GCAGAACAGAAAGTTCAACTGCTTCTTAATTTGGCATCAACTTCATGGAAGAAGAGCG	1090
301	QY	TATGACACATTTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCGAGAGAAAAATT	360
1091	Db	TATGACACATTTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCGAGAGAAAAATT	1150
361	QY	CAGACTATATCTCTCAAGGCATTACTAGTGTACTCAGAAAAATTCAAACTTCAGAAATGAA	420
1151	Db	CAGACTATATCTCTCAAGGCATTACTAGTGTACTCAGAAAAATTCAAACTTCAGAAATGAA	1210

Search completed: June 15, 2003, 20:26:13

Job time : 219 secs





GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:17:33 ; Search time 65 Seconds  
(without alignments)  
2052.375 Million cell updates/sec

Title: US-09-884-987-1\_COPY\_765\_1199

Perfect score: 435

Sequence: 1 aagagaaggaagtagacagaa.....atgaatccaagcttggtc 435

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	857	5	PCT-US95-17083-9
2	435	100.0	920	5	PCT-US95-17083-7
3	435	100.0	1104	5	PCT-US95-17083-3
4	435	100.0	1167	5	PCT-US95-17083-1
5	435	100.0	2471	1	US-08-444-231-18
6	435	100.0	2471	1	US-08-152-443A-18
7	435	100.0	2534	2	US-08-219-237B-1
8	435	100.0	2534	4	US-08-468-560C-1
9	435	100.0	2534	4	US-09-180-100-16
10	435	100.0	2551	4	US-09-290-640-1
11	354	81.4	975	5	PCT-US95-17083-5
12	167.6	38.5	1480	4	US-09-290-640-65
13	50.4	11.6	7218	1	US-08-232-463-14
14	43	9.9	1956	4	US-08-559-898B-1
15	39	9.0	2706	2	US-08-630-822A-61
16	39	9.0	2706	2	US-09-005-069-61
17	39	9.0	2706	4	US-09-171-156A-20
18	38.2	8.8	9244	1	US-08-444-005-14
19	36.8	8.5	9244	4	US-08-961-527-68
20	36.6	8.4	2277	1	US-08-676-967-2
21	36.6	8.4	2277	1	US-08-676-974-2
22	36.6	8.4	2277	2	US-09-098-487-2
23	36	8.3	1000	4	US-09-222-938A-35
24	34.4	7.9	1054	1	US-08-393-985-7
25	33.2	7.6	903	4	US-09-134-001C-1548
26	33.2	7.6	1398	4	US-09-134-001C-1019
27	32.8	7.5	957	1	US-08-349-696-26

c 28	32.8	7.5	957	1	US-08-233-009-26	Sequence 26, Appl
c 29	32.8	7.5	957	1	US-08-560-231-26	Sequence 26, Appl
c 30	32.8	7.5	957	1	US-09-080-704A-26	Sequence 26, Appl
c 31	32.8	7.5	1789	2	US-08-895-521-2	Sequence 2, Appl
c 32	32.8	7.5	1789	3	US-09-235-218-2	Sequence 2, Appl
c 33	32.8	7.5	1962	3	US-08-714-918-18	Sequence 18, Appl
c 34	32.8	7.5	1962	4	US-09-265-315-18	Sequence 18, Appl
c 35	32.8	7.5	1962	4	US-09-266-417-18	Sequence 18, Appl
c 36	32.8	7.5	1056	4	US-09-134-001C-2655	Sequence 2655, Ap
c 37	32.6	7.4	760	2	US-08-474-379C-78	Sequence 78, Appl
c 38	32.4	7.4	760	3	US-09-146-249A-78	Sequence 78, Appl
c 39	32.4	7.4	760	3	US-08-206-188B-78	Sequence 78, Appl
c 40	32.4	7.4	1649	1	US-07-688-352C-35	Sequence 35, Appl
c 41	32.4	7.4	1649	2	US-08-474-379C-35	Sequence 35, Appl
c 42	32.4	7.4	1649	3	US-09-146-249A-35	Sequence 35, Appl
c 43	32.4	7.4	1649	3	US-08-206-188B-35	Sequence 35, Appl
c 44	32.4	7.4	1649	5	PCT-US91-02714-34	Sequence 34, Appl
c 45	32.4	7.4	1649	5	PCT-US91-02714-34	Sequence 34, Appl

#### ALIGNMENTS

RESULT 1  
PCT-US95-17083-9  
; Sequence 9, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT: SECRETED HUMAN FAS ANTIGEN  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 857 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; PCT-US95-17083-9

Query Match	100.0%	Score 435;	DB 5;	Length 857;
Best Local Similarity	100.0%	Pred. No. 3.1e-109;		
Matches 435;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGCAAGGTTCTCAT	60	
Db	286	AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGAGAAAGCAAGGTTCTCAT	345	
QY	61	GAATCTCAACCTTAAATCTGAACAGTGGCAATAATTTATCTGATGTTGACCTGAGT	120	
Db	346	GAATCTCAACCTTAAATCTGAACAGTGGCAATAATTTATCTGATGTTGACCTGAGT	405	
QY	121	AAATATATCACCACATTTGCTGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA	180	
Db	406	AAATATATCACCACATTTGCTGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCA	465	
QY	181	AAGAATGTTGTCATGAAGCCAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	240	
Db	466	AAGAATGTTGTCATGAAGCCAAATAGATGAGATCAAGAATGACAATGTCCAAGACACA	525	
QY	241	GCAGAACAGAAAGTCAACTGCTTGGTAAATGGCATCAACTTTCATGGGAAGAAAGCG	300	
Db	526	GCAGAACAGAAAGTCAACTGCTTGGTAAATGGCATCAACTTTCATGGGAAGAAAGCG	585	
QY	301	TATGACATTCATTAAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAAT	360	
Db	586	TATGACATTCATTAAAGATCTCAAAAAGCAATCTTTGTACTCTTGCAGAGAAAT	645	

OY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 420  
Db 646 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 705  
OY 421 ATCCAAAGCTGGTC 435  
Db 706 ATCCAAAGCTGGTC 720

## RESULT 2

## PCT-US95-17083-7

; Sequence 7, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: 23-DEC-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 920 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

## PCT-US95-17083-7

Query Match 100.0%; Score 435; DB 5; Length 920;

Best Local Similarity 100.0%; Pred. No. 3.2e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAGGAAAGTACAGAAAACATGCGAAGAGGACAGAAAAGGAAAGGAAAGGTTCTCAT 60  
Db 349 AAGAGAAAGGAAAGTACAGAAAACATGCGAAGAGGACAGAAAAGGAAAGGAAAGGTTCTCAT 408  
OY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120  
Db 409 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 468  
OY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
Db 469 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 528  
OY 181 AAGAAATGCTGTCATGAAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 240  
Db 529 AAGAAATGCTGTCATGAAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 588  
OY 241 GCAGAACAGAAAGTTCACACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
Db 589 GCAGAACAGAAAGTTCACACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 648  
OY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGCTGTTGAGAGAAATTT 360  
Db 649 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGCTGTTGAGAGAAATTT 708  
OY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 420  
Db 709 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 768  
OY 421 ATCCAAAGCTGGTC 435  
Db 769 ATCCAAAGCTGGTC 783

## RESULT 3

## PCT-US95-17083-3

; Sequence 3, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: 23-DEC-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1104 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; PCT-US95-17083-3

Query Match 100.0%; Score 435; DB 5; Length 1104;

Best Local Similarity 100.0%; Pred. No. 3.4e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGAGAAAGGAAAGTACAGAAAACATGCGAAGAGGACAGAAAAGGAAAGGTTCTCAT 60  
Db 533 AAGAGAAAGGAAAGTACAGAAAACATGCGAAGAGGACAGAAAAGGAAAGGTTCTCAT 592  
OY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 120  
Db 593 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATATTTATCTGATGTTGACTTGAGT 652  
OY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
Db 653 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 712  
OY 181 AAGAAATGCTGTCATGAAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 240  
Db 713 AAGAAATGCTGTCATGAAAGCCAAATAGATGAGATCAAGAAATGACAATGTCCAAAGACACA 772  
OY 241 GCAGAACAGAAAGTTCACACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 300  
Db 773 GCAGAACAGAAAGTTCACACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCG 832  
OY 301 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGCTGTTGAGAGAAATTT 360  
Db 833 TATGACACATTTGATTAAAGATCTCAAAAAGCCCAATCTTTGCTGTTGAGAGAAATTT 892  
OY 361 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 420  
Db 893 CAGACTATCATCTCCTCAAGGACATTAAGTACTGACTCAGAAAATTCAGAAATGAA 952  
OY 421 ATCCAAAGCTGGTC 435  
Db 953 ATCCAAAGCTGGTC 967

## RESULT 4

## PCT-US95-17083-1

; Sequence 1, Application PC/TUS9517083

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/17083

; FILING DATE: CONCURRENTLY HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: USSN 08/371,263

; FILING DATE: 23-DEC-1994

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1167 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

TOPOLOGY: linear  
PCT-US95-17083-1

Query Match 100.0%; Score 435; DB 5; Length 1167;  
Best Local Similarity 100.0%; Pred. No. 3.4e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60  
DB 596 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 655  
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATGGAATTTATCTGATGTTGACTTGAGT 120  
DB 656 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATGGAATTTATCTGATGTTGACTTGAGT 715  
QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACATTAAGTAAAGTAAAGGCTTTGTTTGA 180  
DB 716 AAATATATCACCACATTTGCTGGAGTCATGACACATTAAGTAAAGTAAAGGCTTTGTTTGA 775  
QY 181 AAGATGCTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 240  
DB 776 AAGATGCTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 835  
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 300  
DB 836 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 895  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTTCGAGAGAAAATT 360  
DB 896 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTTCGAGAGAAAATT 955  
QY 361 CAGACTATCATCCCAAGGACATTAAGTACTAGTACTCAGAGAAAATTCAAACTTCAGAAATGAA 420  
DB 956 CAGACTATCATCCCAAGGACATTAAGTACTAGTACTCAGAGAAAATTCAAACTTCAGAAATGAA 1015  
QY 421 ATCCAAAGCTTGGTC 435  
DB 1016 ATCCAAAGCTTGGTC 1030

## RESULT 5

US-08-444-231-18  
; Sequence 18, Application US/08444231  
; Patent No. 5652210

## GENERAL INFORMATION:

; APPLICANT: BARR, PHILIP J.  
; APPLICANT: SHAPIRO, JOHN P.  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22

## CORRESPONDENCE ADDRESS:

; ADDRESS: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA

; ZIP: 94304-1018

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0 Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444/231

; FILING DATE: 18-MAY-1995

## CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/152-443

; FILING DATE: 15-NOV-1993

## ATTORNEY/AGENT INFORMATION:

; NAME: LEHNHARDT, SUSAN K.

; REGISTRATION NUMBER: 33,943

; REFERENCE/DOCKET NUMBER: 23647-20006.00  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 813-5600

; TELEFAX: (415) 494-0792

; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2471 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 195..1136

; FEATURE:

; NAME/KEY: mat\_peptide

; LOCATION: 243

; US-08-444-231-18

Query Match 100.0%; Score 435; DB 1; Length 2471;

Best Local Similarity 100.0%; Pred. No. 4.4e-109;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60  
DB 702 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 761  
QY 61 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATGGAATTTATCTGATGTTGACTTGAGT 120  
DB 762 GAATCTCCAACTTAAATCCTGAAACAGTGGCAATGGAATTTATCTGATGTTGACTTGAGT 821  
QY 121 AAATATATCACCACATTTGCTGGAGTCATGACACATTAAGTAAAGGCTTTGTTTGA 180  
DB 822 AAATATATCACCACATTTGCTGGAGTCATGACACATTAAGTAAAGGCTTTGTTTGA 881  
QY 181 AAGATGCTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 240  
DB 882 AAGATGCTGTCAATGAAGCCAAATATAGATGAGATCAAGATGACAATGTCCAAGACACA 941  
QY 241 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 300  
DB 942 GCAGAACAGAAAGTTCAACTGCTTCTGTAATTTGGCATCAACTTTCATGGAAAGAAAGAGCG 1001  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTTCGAGAGAAAATT 360  
DB 1002 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTTCGAGAGAAAATT 1061  
QY 361 CAGACTATCATCCCAAGGACATTAAGTACTAGTACTCAGAGAAAATTCAAACTTCAGAAATGAA 420  
DB 1062 CAGACTATCATCCCAAGGACATTAAGTACTAGTACTCAGAGAAAATTCAAACTTCAGAAATGAA 1121  
QY 421 ATCCAAAGCTTGGTC 435  
DB 1122 ATCCAAAGCTTGGTC 1136

## RESULT 6

US-08-152-443A-18

; Sequence 18, Application US/08152443A

; Patent No. 5663070

## GENERAL INFORMATION:

; APPLICANT: BARR, PHILIP J.

; APPLICANT: SHAPIRO, JOHN P.

; APPLICANT: KIEFER, MICHAEL C.

; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 22

## CORRESPONDENCE ADDRESS:

; ADDRESS: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/152,443A  
FILING DATE: 15-NOV-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 195..1136  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 243  
US-08-152-443A-18

Query Match 100.0%; Score 435; DB 1; Length 2471;  
Best Local Similarity 100.0%; Pred. No. 4.4e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 60  
Db |  
Qy 702 AAGAGAAAGGAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCAT 761  
Db |  
Qy 61 GAATCTCAACCTTAATCTGGAACAGTGCAGCAATTAATCTGATGTTGACTTCAGT 120  
Db |  
Qy 762 GAATCTCAACCTTAATCTGGAACAGTGCAGCAATTAATCTGATGTTGACTTCAGT 821  
Db |  
Qy 121 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 180  
Db |  
Qy 822 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 881  
Db |  
Qy 181 AAGAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGATGCAAGACACA 240  
Db |  
Qy 882 AAGAATGGTCTCAATGAAGCCAAATAGATGAGATGACAAATGATGCAAGACACA 941  
Db |  
Qy 241 GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCG 300  
Db |  
Qy 942 GCAGAACAGAAAGTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCG 1001  
Db |  
Qy 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTTACTCTTGACAGAAAT 360  
Db |  
Qy 1002 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTTACTCTTGACAGAAAT 1061  
Db |  
Qy 361 CAGACTATATCTCTCAAGGACATTAAGTACTGACTCAGAAATTCAACTTCAGAAATGAA 420  
Db |  
Qy 1062 CAGACTATATCTCTCAAGGACATTAAGTACTGACTCAGAAATTCAACTTCAGAAATGAA 1121  
Db |  
Qy 421 ATCCAAGCTTGGTC 435  
Db 1122 ATCCAAGCTTGGTC 1136

## RESULT 7

US-08-219-237B-1  
; Sequence 1, Application US/08219237B  
; Patent No. 5674546

GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu  
APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin  
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James W. Hellwege  
STREET: P.O. Box 2266 Eads Station  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/219,237B  
FILING DATE: 28-MAR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US-07/872,129  
FILING DATE: 22-APR-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: James W. Hellwege  
REGISTRATION NUMBER: 28,808  
REFERENCE/DOCKET NUMBER: 516762  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2534 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
LIBRARY: pCEV4  
CLONE: clone pf58  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 195..1202  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 195..242  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 243..1199  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 1831..1836  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 2352..2357  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 2518..2523  
IDENTIFICATION METHOD: by similarity with known sequence or  
IDENTIFICATION METHOD: to an established consensus  
US-08-219-237B-1

Query Match 100.08; Score 435; DB 2; Length 2534;  
Best Local Similarity 100.08; Pred. No. 4.5e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAAGAACGACAGAAAAGGAAAGGAAAGGTTCTCAT 60  
DB 765 AAGAGAAAGGAGTACAGAAAACATGCAAGAACGACAGAAAAGGAAAGGTTCTCAT 824

QY 61 GAATCTCAACCTTAAATCTGCAAGAGTGGCAATATTTATCTGTGTTGACTTGAGT 120  
DB 825 GAATCTCAACCTTAAATCTGCAAGAGTGGCAATATTTATCTGTGTTGACTTGAGT 884

QY 121 AAATATATCACCACCTATTTGCTGGAGTCAATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
DB 885 AAATATATCACCACCTATTTGCTGGAGTCAATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 944

QY 181 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATGCAATGCAATGTCACAGACACA 240  
DB 945 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATGCAATGCAATGTCACAGACACA 1004

QY 241 GCAGAACAGAAAGTTCACCTCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAACGG 300  
DB 1005 GCAGAACAGAAAGTTCACCTCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAACGG 1064

QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGGCAGAGAAATTT 360  
DB 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGGCAGAGAAATTT 1124

QY 361 CAGACTATATCTCCCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 420  
DB 1125 CAGACTATATCTCCCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 1184

QY 421 ATCCAAAGCTTGGTC 435  
DB 1185 ATCCAAAGCTTGGTC 1199

## RESULT 8

US-08-468-560C-1  
; Sequence 1 Application US/08468560C  
; Patent No. 627098

GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu

APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin

TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
STREET: P.O. BOX 747

CITY: FALLS CHURCH  
STATE: VA

COUNTRY: USA  
ZIP: 22040-0747

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,560C  
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR., GERLAD M.  
REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 20-4393P  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 1:

TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE

SEQUENCE CHARACTERISTICS:  
LENGTH: 2534 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 195..1202  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 195..242  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 243..1199  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 1831..1836  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 2352..2357  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 2518..2532  
US-08-468-560C-1

Query Match 100.08; Score 435; DB 4; Length 2534;

Best Local Similarity 100.08; Pred. No. 4.5e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAAACATGCAAGAACGACAGAAAAGGAAAGGTTCTCAT 60  
DB 765 AAGAGAAAGGAGTACAGAAAACATGCAAGAACGACAGAAAAGGAAAGGTTCTCAT 824

QY 61 GAATCTCAACCTTAAATCTGCAAGAGTGGCAATATTTATCTGTGTTGACTTGAGT 120  
DB 825 GAATCTCAACCTTAAATCTGCAAGAGTGGCAATATTTATCTGTGTTGACTTGAGT 884

QY 121 AAATATATCACCACCTATTTGCTGGAGTCAATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
DB 885 AAATATATCACCACCTATTTGCTGGAGTCAATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 944

QY 181 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATGCAATGCAATGTCACAGACACA 240  
DB 945 AAGAAATGCTGTCATGAAGCCAAATAGATGAGATGCAATGCAATGTCACAGACACA 1004

QY 241 GCAGAACAGAAAGTTCACCTCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAACGG 300  
DB 1005 GCAGAACAGAAAGTTCACCTCTGTAATTTGGCATCAACTTCATGGAAAGAAAGAACGG 1064

QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGGCAGAGAAATTT 360  
DB 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCCAATCTTTGACTCTTGGCAGAGAAATTT 1124

QY 361 CAGACTATATCTCCCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 420  
DB 1125 CAGACTATATCTCCCAAGGACATTTACTAGTACTCAGAAAATTCAAAATTCAGAAATGAA 1184

QY 421 ATCCAAAGCTTGGTC 435  
DB 1185 ATCCAAAGCTTGGTC 1199

## RESULT 9

US-09-180-100-16  
; Sequence 16 Application US/09180100

GENERAL INFORMATION:  
PATENT NO. 6306395

APPLICANT: NAKAMURA, No. 630639510  
APPLICANT: NAGATA, Shigekazu

FILE REFERENCE: 1110-207P  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/JP97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 16  
LENGTH: 2534  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-180-100-16

Query Match 100.0%; Score 435; DB 4; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 4.5e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60  
Db 765 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 824  
Qy 61 GAATCTCCACCTTAAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120  
Db 825 GAATCTCCACCTTAAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 884  
Qy 121 AAATATATCACCACCTATTGCTGGAGTCATGACACATTAAGTCAAGTTAAAGGCTTTGTTGCGA 180  
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACATTAAGTCAAGTTAAAGGCTTTGTTGCGA 944  
Qy 181 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 240  
Db 945 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 1004  
Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300  
Db 1005 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1064  
Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAATT 360  
Db 1065 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAATT 1124  
Qy 361 CAGACTATCATCTCCAAAGGACATTAAGTACTGACTCAGAAAATTCAAAATTCAGAAATGAA 420  
Db 1125 CAGACTATCATCTCCAAAGGACATTAAGTACTGACTCAGAAAATTCAAAATTCAGAAATGAA 1184  
Qy 421 ATCCAAAGCTTGGTC 435  
Db 1185 ATCCAAAGCTTGGTC 1199

RESULT 10  
US-09-290-640-1  
Sequence 1, Application US/09290640  
Patent No. 6204055  
GENERAL INFORMATION:  
APPLICANT: Marcuss, Eric G.  
APPLICANT: Dean, Nicholas M.  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-0351  
CURRENT APPLICATION NUMBER: US/09/290,640  
CURRENT FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 85  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
LENGTH: 2551  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (221)..(1228)  
PUBLICATION INFORMATION:  
JOURNAL: J. Biol. Chem.  
VOLUME: 267

ISSUE: 15  
PAGES: 10709-10715  
DATE: 1992-05-25  
DATABASE ACCESSION NUMBER: X63717/Genbank  
DATABASE ENTRY DATE: 1996-07-19  
US-09-290-640-1

Query Match 100.0%; Score 435; DB 4; Length 2551;  
Best Local Similarity 100.0%; Pred. No. 4.5e-109;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 60  
Db 791 AAGAGAAGGAAGTACAGAAACATCGAGAAAGCAGACAGAAAGGAAAGGTTCTCAT 850  
Qy 61 GAATCTCCACCTTAAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 120  
Db 851 GAATCTCCACCTTAAATCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTGAGT 910  
Qy 121 AAATATATCACCACCTATTGCTGGAGTCATGACACATTAAGTCAAGTTAAAGGCTTTGTTGCGA 180  
Db 911 AAATATATCACCACCTATTGCTGGAGTCATGACACATTAAGTCAAGTTAAAGGCTTTGTTGCGA 970  
Qy 181 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 240  
Db 971 AAGAAATGCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACA 1030  
Qy 241 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300  
Db 1031 GCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 1090  
Qy 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAATT 360  
Db 1091 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTGCAGAGAAAATT 1150  
Qy 361 CAGACTATCATCTCCAAAGGACATTAAGTACTGACTCAGAAAATTCAAAATTCAGAAATGAA 420  
Db 1151 CAGACTATCATCTCCAAAGGACATTAAGTACTGACTCAGAAAATTCAAAATTCAGAAATGAA 1210  
Qy 421 ATCCAAAGCTTGGTC 435  
Db 1211 ATCCAAAGCTTGGTC 1225

RESULT 11  
PCT-US95-17083-5  
Sequence 5, Application PC/TUS9517083  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
NUMBER OF SEQUENCES: 16  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17083  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/371,263  
FILING DATE: 23-DEC-1994  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 975 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-17083-5

Query Match 81.4%; Score 354; DB 5; Length 975;  
Best Local Similarity 100.0%; Pred. No. 3.1e-87;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACCACCTATTGCT 141  
Db 485 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCACCACCTATTGCT 544

[illegible]

**RESULT 12**

US-09-290-640-65  
 ; Sequence 65, Application US/09290640  
 ; Patent No. 6204055  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Marcussen, Eric G.  
 ; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
 ; FILE REFERENCE: ISPH-0351  
 ; CURRENT APPLICATION NUMBER: US/09/290,640  
 ; CURRENT FILING DATE: 1999-04-12  
 ; NUMBER OF SEQ ID NOS: 85  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 65  
 ; LENGTH: 1480  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (50)..(1033)  
 ; PUBLICATION INFORMATION:  
 ; JOURNAL: J. Immunol.  
 ; VOLUME: 148  
 ; PAGES: 1274-1297  
 ; DATE: 1992-02-15  
 ; DATABASE ACCESSION NUMBER: M83649/Genbank  
 ; DATABASE ENTRY DATE: 1994-04-18  
 US-09-290-640-65

Dd    863   TGCTGGTACCAATCTCATGGAAGAGTGATGCATATCAAGAATTAAATCAAGGTCTCCAA    922

Qy     328   AAAGCCCAATTTTGTACTCTTCGAGAGAAAATTCAGACATACTATCATCCTCAAGGACATTACT    387  
         |       |       |       |       |       |       |       |       |       |  
Dd    923   AAAGCCCAATGTGCGAGAACCTTAGATAAATTTTCAGGACATGTCGAGAAGGACCTTGG    982

Qy     388   AGTGCATCTCAGAAAATTCAAACTTCAGANAATGAATCCAAGCTTGG    433  
         |       |       |       |       |       |       |       |       |       |

Dd    983   AATCAACCCCAGACACTGGAATGAANAATGAAGGACAATGTCTGG    1028

RESULT 13.

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/08/232.463

; APPLICATION NUMBER: US/08/232.463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: ptzgmt-F1s

; PS-US-08-232-463-14

	Query Match	11.6%	Score 50.4;	DB 1;	Length 7218;
	Best Local Similarity	4.2%;	Pred. No. 0.00015;	Mismatches 15;	Conservative 200;
				Indels 0;	Gaps 0;
Qy	1	AACAGAAAGCAAGTACAGAAAACATGCAGAACGACAGAAGGAACCAAGTTCTCAT	60		
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Dd	1394	RRR	1355		
		: :			
Qy	61	GAATCTCCAACCTTAATCTCGAACAAGTCGCGCAATAATTATCTGATGTGGACTTGAGT	120		
		: :			
Dd	1334	RRR	1275		
		: :			
Qy	121	AAATATATACCACCTATTGCTGGAGTCATGACACATAAGCTTAAGGCTTGTTTCGA	180		





QY	244	GAAAGAAAGTTCAACTGCTTCGTAATGGCATCAACTTCATGGAAGAAAGAGCGTAT	303
Db	2414	GAACTTAAAGAAAGAACTTGAAGAAATCTCGTCATATTCAAGAAATGGAAGAAAGA	2473
QY	304	GACACATTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTCAG	363
Db	2474	GAAAGTTTGGTTCATCAGCTACAAATTCGATTAGCTAGAGCTGATTCAGAGGCAATTGGCG	2533
QY	364	ACTATCATCTCAAGGACATTTACTAGTGAATCAAGAAATTCAGAAATGAAATC	423
Db	2534	AGATCAATAGCTGATGAAAGTATAGCTGATTAGAAAGGAAAGAAAGAACTATGAAGGAATTA	2593
QY	424	CAA	426
Db	2594	GAA	2596

Search completed: June 15, 2003, 21:13:05  
Job time : 66 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 20:47:53 ; Search time 126 Seconds  
(without alignments)  
4999.257 Million cell updates/sec

Title: US-09-884-987-1\_COPY\_765\_1199

Perfect score: 435

Sequence: 1 aagagaaaggagtagtacagaa.....atgaataccaagcttgctc 435

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications, NA:\*
- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
  - 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
  - 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
  - 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*
  - 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
  - 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*
  - 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
  - 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	836	10	US-09-802-669-102
2	435	100.0	2534	10	US-09-949-713-16
3	435	100.0	2534	10	US-09-884-987-1
4	435	100.0	2551	10	US-09-802-669-1
C 5	435	100.0	8282	9	US-09-966-976A-7
C 6	435	100.0	8282	9	US-09-963-206B-7
C 7	435	100.0	8345	9	US-09-966-976A-8
C 8	435	100.0	8345	9	US-09-963-206B-8
9	404.2	92.9	490	9	US-09-918-995-17119
10	394.4	90.7	398	10	US-09-867-701-2490
11	383.6	88.2	460	10	US-09-867-701-3156
12	354	81.4	975	9	US-09-954-531-998
13	330	75.9	1840	10	US-09-802-669-101
14	302	69.4	489	9	US-09-918-995-13045
15	302	69.4	496	9	US-09-918-995-15171
16	224.8	51.7	447	9	US-09-918-995-7395
17	167.6	38.5	1480	10	US-09-802-669-65
18	83.4	19.2	338	10	US-09-802-669-99
19	43	9.9	1956	10	US-09-351-794A-1

ALIGNMENTS

RESULT 1

US-09-802-669-102

; Sequence 102, Application US/09802669

; Patent No. US20020004490A1

; GENERAL INFORMATION:

; APPLICANT: Dean, Nicholas M.

; APPLICANT: Marcussen, Eric G.

; APPLICANT: Wyatt, Jacqueline

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

; FILE REFERENCE: ISPH-545

; CURRENT APPLICATION NUMBER: US/09-802,669

; CURRENT FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: US/09/665,615

; PRIOR FILING DATE: 2000-09-19

; PRIOR APPLICATION NUMBER: US/09/290,640

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 180

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 102

; LENGTH: 836

; TYPE: DNA

; ORGANISM: Homo sapiens.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(399)

US-09-802-669-102

Query Match 100.0%; Score 435; DB 10; Length 836;

Best Local Similarity 100.0%; Pred. No. 8e-104;

Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	AAGAGAAAGGAGTAGTACAGAAAACATGCAGAAAGCAGACAGAAAGCAAGGTTCTCAT	60
Db	399	AGAGAAAGGAGTAGTACAGAAAACATGCAGAAAGCAGACAGAAAGCAAGGTTCTCAT	458
QY	61	GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTCTGATGTTGACTTGAGT	120
Db	459	GAATCTCCAACTTAAATCCTGAAACAGTGGCAATTAATTTCTGATGTTGACTTGAGT	518
QY	121	AAATATATACCACTATTCTGAGTTCATGACACTAAGTCAAGTTAAAGCTTTGTTCCA	180

Db 519 AAATATATACACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 578  
QY 181 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATCTCCAGACACA 240  
Db 579 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATCTCCAGACACA 638  
QY 241 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 300  
Db 639 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 698  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360  
Db 699 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 758  
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAACTTCAGAAATGAA 420  
Db 759 CAGACTATCATCTCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAACTTCAGAAATGAA 818  
QY 421 ATCCAAAGCTTGGTC 435  
Db 819 ATCCAAAGCTTGGTC 833

## RESULT 2

US-09-949-713-16  
; Sequence 16, Application US/09949713  
; Patent No. US20020044944A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, No. US20020044944A1  
; APPLICANT: NAKAMURA, Shigekazu  
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
; FILE REFERENCE: 1110-207P  
; CURRENT APPLICATION NUMBER: US/09/949,713  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US/09/180,100  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: PCT/JP97/01502  
; PRIOR FILING DATE: 1997-05-01  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 2534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-949-713-16

Query Match 100.0%; Score 435; DB 10; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 1.4e-103;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 60  
Db 765 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 824  
QY 61 GAATCTCAACCTTAAATCTTGAACAGCTGCAATTAATTTATCTGATGTTGACTTGAGT 120  
Db 825 GAATCTCAACCTTAAATCTTGAACAGCTGCAATTAATTTATCTGATGTTGACTTGAGT 884  
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 180  
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 944  
QY 181 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATTTGTTGGA 240  
Db 945 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATTTGTTGGA 1004  
QY 241 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 300  
Db 1005 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 1064  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360  
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 1124

QY 361 CAGACTATCATCTCAAGGACATTTACTAGTACTGAGAAATTTCAAACTTCAGAAATGAA 420  
Db 1125 CAGACTATCATCTCAAGGACATTTACTAGTACTGAGAAATTTCAAACTTCAGAAATGAA 1184  
QY 421 ATCCAAAGCTTGGTC 435  
Db 1185 ATCCAAAGCTTGGTC 1199

## RESULT 3

US-09-884-987-1  
; Sequence 1, Application US/09884987  
; Patent No. US20020102653A1  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu et al  
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN  
; FILE REFERENCE: 0020-4877P  
; CURRENT APPLICATION NUMBER: US/09/884,987  
; CURRENT FILING DATE: 2001-06-21  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn/version 3.0  
; SEQ ID NO 1  
; LENGTH: 2534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: (1831)..(1836)  
; NAME/KEY: mat\_peptide  
; LOCATION: (243)..()  
; NAME/KEY: sig\_peptide  
; LOCATION: (195)..(242)  
; NAME/KEY: CDS  
; LOCATION: (195)..(1199)  
; NAME/KEY: polyA\_site  
; LOCATION: (2352)..(2357)  
; NAME/KEY: polyA\_site  
; LOCATION: (2516)..(2532)  
US-09-884-987-1

Query Match 100.0%; Score 435; DB 10; Length 2534;  
Best Local Similarity 100.0%; Pred. No. 1.4e-103;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 60  
Db 765 AAGAGAAAGGAGTACAGAAAACATGCGAAGACGACAGAAAGGAAACCAAGGTTCTCAT 824  
QY 61 GAATCTCAACCTTAAATCTTGAACAGCTGCAATTAATTTATCTGATGTTGACTTGAGT 120  
Db 825 GAATCTCAACCTTAAATCTTGAACAGCTGCAATTAATTTATCTGATGTTGACTTGAGT 884  
QY 121 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 180  
Db 885 AAATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGA 944  
QY 181 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATTTGTTGGA 240  
Db 945 AAGATGTTGTCATGAAGCCAAATAGATGAGATCAAGATGCAATTTGTTGGA 1004  
QY 241 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 300  
Db 1005 GCAGAACAGAAAGTTCAACTGCTTGGTAATTTGGCATCAACTTTCATGGAAAGAAAGCG 1064  
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 360  
Db 1065 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGACTCTTTCAGAGAGAAAT 1124  
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAACTTCAGAAATGAA 420  
Db 1125 CAGACTATCATCTCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAACTTCAGAAATGAA 1184



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: PRIOR FILING DATE: 1998-05-12
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: Patent In Version 3.1
: SEQ ID NO 8
: LENGTH: 8345
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: synthetic
US-09-966-976A-8

Query Match 100.0%; Score 435; DB 9; Length 8345;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 AAGAGAAGCAAGTACAGAAACATCGAAGAACACAGAAAGCAAGAAAGCAAGCTTCTCAT 60
Db 4353 AAGAGAAGCAAGTACAGAAACATCGAAGAACACAGAAAGCAAGAAAGCAAGCTTCTCAT 4294
QY 61 GAATCTCCAAACCTTAATCTCGAAACAGTGGCCAAATAATTTATCTGATGTGACTTGAGT 120
Db 4293 GAATCTCCAAACCTTAATCTCGAAACAGTGGCCAAATAATTTATCTGATGTGACTTGAGT 4234
QY 121 AATATATACCACTATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCTGA 180
Db 4233 AATATATACCACTATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCTGA 4174
QY 181 AAGAAATGGTCTCAATGAAGCCAAANTAGATGAGATCAAGAATGCAATGTCCAAAGACACA 240
Db 4173 AAGAAATGGTCTCAATGAAGCCAAANTAGATGAGATCAAGAATGCAATGTCCAAAGACACA 4114
QY 241 GCAGACAGAAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAGAAGCG 300
Db 4113 GCAGACAGAAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAGAAGCG 4054
QY 301 TATGACACATTTGATTTAAAGATCTCAAAAAAGCCAACTTTTGTACTCTTCGACAGAAAAATT 360
Db 4053 TATGACACATTTGATTTAAAGATCTCAAAAAAGCCAACTTTTGTACTCTTCGACAGAAAAATT 3994
QY 361 CAGACTATCATCTCTCAAGGACATTTACTAGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 420
Db 3993 CAGACTATCATCTCTCAAGGACATTTACTAGTGACTCAGAAAAATTCAAACTTCAGAAATGAA 3934
QY 421 ATCCAAAGCTTGGTC 435
Db 3933 ATCCAAAGCTTGGTC 3919

RESULT 8
US-09-963-206B-8/c
: Sequence 8, Application US/09963206B
: Patent No. US20020123076A1
: GENERAL INFORMATION:
: APPLICANT: Ferrick, David A.
: APPLICANT: Swift, Susan E.
: APPLICANT: Armstrong, Randall
: APPLICANT: Fox, Bryan
: TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and
: FILE OF INVENTION: Secretion and Switch Rearrangement
: FILE REFERENCE: A-66038-3/RMS/JJD/DLR
: CURRENT APPLICATION NUMBER: US/09/963, 206B
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 09/076,624
: PRIOR FILING DATE: 1998-05-12
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: Patent In Version 3.1
: SEQ ID NO 8
: LENGTH: 8345
: TYPE: DNA
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: synthetic
US-09-963-206B-8

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Query Match      100.0%; Score 435; DB 10; Length 8345;
Best Local Similarity 100.0%; Pred. No. 2.6e-103;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAATCTCAACCTTAAATCTGAAACAGTGGCAGTAAATTTATCTGATGTTGACTTGAGT 120
DB 4293 GAATCTCAACCTTAAATCTGAAACAGTGGCAGTAAATTTATCTGATGTTGACTTGAGT 4234
QY 121 AATATATACCACTATTGCTGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGGA 180
DB 4233 AATATATACCACTATTGCTGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGGA 4174
QY 181 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCACAGACACA 240
DB 4173 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCACAGACACA 4114
QY 241 GCAGAACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300
DB 4113 GCAGAACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 4054
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 360
DB 4053 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 3994
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAATTCACAAATTCAGAAATGAA 420
DB 3993 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAATTCACAAATTCAGAAATGAA 3934
QY 421 ATCCAAAGCTTGTC 435
DB 3933 ATCCAAAGCTTGTC 3919

RESULT 9
US-09-918-995-17119
; Sequence 17119, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR FILING DATE: US/09/235,076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17119
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(490)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-17119

Query Match      92.9%; Score 404.2; DB 9; Length 490;
Best Local Similarity 97.9%; Pred. No. 6.7e-96;
Matches 420; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 AAGAGAAAGGAAGTACAGAGAAACATGACAGAAAGCAGAGAAAGGAAACCAAGGTTCTCAT 60
DB 63 AAGAGAAAGGAAGTACAGAGAAACATGCA-TTTCACAGAAATGGAACCAAGGCTCTCAT 121
QY 61 GAATCTCAACCTTAAATCTGAAACAGTGGCAGTAAATTTATCTGATGTTGACTTGAGT 120
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DB 122 GAATCTCCAACTTAGATCTCTGAAACAGAGGCAATTAATTTATCTGATGTTGACTTCAGT 181
QY 121 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGGA 180
|||||
DB 182 AATATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCTTAAAGGCTTTGTTGGA 241
QY 181 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCACAGACACA 240
|||||
DB 242 AAGATGGTGTCAATGAAGCCAAATAGATGACATCAAGAAATGACAAATGTCACAGACACA 301
QY 241 GCAGAACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 300
|||||
DB 302 GCAGAACAGAAAGTTCACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAGCG 361
QY 301 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 360
|||||
DB 362 TATGACACATTTGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTT 421
QY 361 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAATTCACAAATTCAGAAATGAA 420
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DB 422 CAGACTATCATCTCAAGGACATTTACTAGTGACTCAGAAATTCACAAATTCAGAAATGAA 481
QY 421 ATCCAAAGC 429
DB 482 ATCCAAAGC 490

RESULT 10
US-09-867-701-2490
; Sequence 2490, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2490
; LENGTH: 398
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(398)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-2490

Query Match      90.7%; Score 394.4; DB 10; Length 398;
Best Local Similarity 99.5%; Pred. No. 2.2e-93;
Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 AGCACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCTCTGAAACAGTGG 91
DB 1 AGCACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACCTTAAATCTCTGAAACAGTGG 60
QY 92 CAATAAATTTATCTGATGTTGACTTGAGTAAATATATATCACCACATATTGCTGGAGTCA 151
DB 61 CAATAAATTTATCTGATGTTGACTTGAGTAAATATATATCACCACATATTGCTGGAGTCA 120
QY 152 CACTAAGTCAAGTAAAGGCTTTGTCGAAAGAAATGTCATCAATGAAGCCAAATAGATG 211
DB 121 CACTAAGTCAAGTAAAGGCTTTGTCGAAAGAAATGTCATCAATGAAGCCAAATAGATG 180
QY 212 AGATCAAGAAATGACAAATGTCACAGACACAGCAGACAGAAAGTTCACCTCTCGTAAT 271
DB 181 AGATCAAGAAATGACAAATGTCACAGACACAGCAGACAGAAAGTTCACCTCTCGTAAT 240
QY 272 GCATCAACTTTCATGGAAGAAAGAGCGGTATGACACATTTGATTAAGATCTCAAAAAG 331
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Db 241 GCATCAACTTCATGGAAGAAGCGGTATGACACATTTGATTAAAGATCTCAAAAAAG 300  
QY 332 CCAATCTTTGTACTCTTGAGAGAAAAATTCAGACTATATCTCTCAAGGACATTACTAGTG 391  
Db 301 CCAATCTTTGTACTCTTGAGAGAAAAATTCAGACTATATCTCTCAAGGACATTACTAGTG 360  
QY 392 ACTCAGAAAATTCAAACTTTCAGAAATGAAATCCAAAG 428  
Db 361 ACTCGGAAAATTCAACTTCAGAAATGAAATCCAAAG 397

RESULT 11

US-09-867-701-3156  
; Sequence 3156, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Agiate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; NUMBER OF SEQ ID NOS: 2001-05-29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3156  
; LENGTH: 460  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-3156

Query Match 88.2%; Score 383.6; DB 10; Length 460;  
Best Local Similarity 99.0%; Pred. No. 1.6e-90;  
Matches 386; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 AACCAAGGTTCTCATGAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCT 105  
Db 1 AACCAAGGTTCTCATGAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCT 60  
QY 106 GATGTTGACTTGAGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 165  
Db 61 GATGTTGACTTGAGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 120  
QY 166 AAAGCTTTGTTGGAAGAAGTGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGAC 225  
Db 121 AAAGCTTTGTTGGAAGAAGTGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGAC 180  
QY 226 AATGTCCAGACACAGCAGACAGAAAGTTCAACTGCTTCGTTAAATGGCATCAACTTCAT 285  
Db 181 AATGTCCAGACACAGCAGACAGAAAGTTCAACTGCTTCGTTAAATGGCATCAACTTCAT 240  
QY 286 GGAAGAAGAAGCGTGTGACACATGATTAAAGATCTCAAAAAAGCCAATCTTTGTACT 345  
Db 241 GGAAGAAGAATTCGTATGACACATGATTAAAGATCTCAAAAAAGCCAATCTTTGTACT 300  
QY 346 CTTCAGAGAAAATTCAGACTATATCTCTCAAGGACATTACTAGTACTCAGAAAATTC 405  
Db 301 CTTCAGAGAAAATTCAGACTATATCTCTCAAGGACATTACTAGTACTCAGAAAATTC 360  
QY 406 AACTTCAGAAAATGAAATCCAAAGCTTGGTC 435  
Db 361 AACTTCAGAAAATGAAATCCAAAGCTTGGTC 390

RESULT 12

US-09-954-531-998  
; Sequence 998, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand

; TITLE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 998  
; LENGTH: 975  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-954-531-998

Query Match 81.4%; Score 354; DB 9; Length 975;  
Best Local Similarity 100.0%; Pred. No. 1.2e-82;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGGTAAATATATATACCACTATTGCT 141  
Db 485 GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGGTAAATATATATACCACTATTGCT 544  
QY 142 GGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGATGGTGTCAATGAAGCC 201  
Db 545 GGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGATGGTGTCAATGAAGCC 604  
QY 202 AAATAGATGATCAAGATGCAATGTCCAGACACAGCAGACAGAAAGTTCAAGTG 261  
Db 605 AAATAGATGATCAAGATGCAATGTCCAGACACAGCAGACAGAAAGTTCAAGTG 664  
QY 262 CTTCGTAATGGCATCAACTTCATGGAAGAAGGCGTATGACACATTGATTAAAGAT 321  
Db 665 CTTCGTAATGGCATCAACTTCATGGAAGAAGGCGTATGACACATTGATTAAAGAT 724  
QY 322 CTCAAAAAGCCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATCATCTCAAGGAC 381  
Db 775 CTCAAAAAGCCAATCTTTGTACTCTTCAGAGAAAATTCAGACTATCATCTCAAGGAC 784  
QY 382 ATTACTAGTACTCAGAAAATTCAACTTCAGAAAATGAAATCCAAAGCTTGGTC 435  
Db 785 ATTACTAGTACTCAGAAAATTCAACTTCAGAAAATGAAATCCAAAGCTTGGTC 838

RESULT 13

US-09-802-669-101  
; Sequence 101, Application US/09802669  
; Patent No. US2002000490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcusson, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US/09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 101  
; LENGTH: 1840  
; TYPE: DNA



ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (95)...(426)  
US-09-802-669-101

Query Match  
Best Local Similarity 75.9%; Score 330; DB 10; Length 1840;  
Matches 333; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 98 ATTATCTGATGTTGACCTTGAAGTAATATATACACACATATGCTGGAGTCAATGACACTAA 157  
|||||  
DB 86 ATTTTCAGATGTTGACCTTGTAAATATATACACACATATGCTGGAGTCAATGACACTAT 145  
|||||

QY 158 GTCAGTTAAAGGCTTTGTTGAAAGAAATGTTGTAATGAAGCCCAAAATAGATGAGATCA 217  
|||||  
DB 146 GTCAGTTAAAGGCTTTGTTGAAAGAAATGTTGTAATGAAGCCCAAAATAGATGAGATCA 205  
|||||

QY 218 AGAATGACAATGTCACAGACACAGCAGACAGAAAGTTCAACTGCTTGTAAATGGCATC 277  
|||||  
DB 206 AGAATGACAATGTCACAGACACAGCAGACAGAAAGTTCAACTGCTTGTAAATGGCATC 265  
|||||

QY 278 AACTTCATGGAAGAAAGGCTATGACACATTCATTAAGATCTCAAAAAAGCCAATC 337  
|||||  
DB 266 AACTTCATGGAAGAAAGGCTATGACACATTCATTAAGATCTCAAAAAAGCCAATC 325  
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QY 338 TTGTACTCTTCGACAGAAAATTCAGATATCATCTCAAGGACATTAATAGTACTGACTCAG 397  
|||||  
DB 326 TTGTACTCTTCGACAGAAAATTCAGATATCATCTCAAGGACATTAATAGTACTGACTCAG 385  
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QY 398 AAAATTCAACTTCAGAAATGAATCCAAAGCTTGGTC 435  
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DB 386 AAAATTCAACTTCAGAAATGAATCCAAAGCTTGGTC 423  
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RESULT 14  
US-09-918-995-13045  
; Sequence 13045, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13045  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(489)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-13045

Query Match  
Best Local Similarity 69.4%; Score 302; DB 9; Length 489;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 CTATTGCTGGAGTCAATGACACTCAAGTTAAAGGCTTTGTTGAAAGAAATGCTGTCATCA 193  
|||||  
DB 55 CTATTGCTGGAGTCAATGACACTCAAGTTAAAGGCTTTGTTGAAAGAAATGCTGTCATCA 114  
|||||

QY 194 ATGAAGCCCAAAATAGATGAGATCAAGAAATGCAATGTCCAGACACAGCAGAACAGAAAG 253  
|||||  
DB 115 ATGAAGCCCAAAATAGATGAGATGCAATGTCCAGACACAGCAGAACAGAAAG 174  
|||||

QY 254 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATGACACTTGA 313  
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Search completed: June 15, 2003, 22:03:40  
Job time : 134 secs

Db 175 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATGACACTTGA 234  
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QY 314 TTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCC 373  
|||||

Db 235 TTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCC 294  
|||||

QY 374 TCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAATTCAGAAATGAAATCCAAAGCTTGG 433  
|||||

Db 295 TCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAATTCAGAAATGAAATCCAAAGCTTGG 354  
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QY 434 TC 435  
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Db 355 TC 356  
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RESULT 15  
US-09-918-995-15171  
; Sequence 15171, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15171  
; LENGTH: 496  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(496)  
OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-15171

Query Match  
Best Local Similarity 69.4%; Score 302; DB 9; Length 496;  
Matches 302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 CTATTGCTGGAGTCAATGACACTCAAGTTAAAGGCTTTGTTGAAAGAAATGCTGTCATCA 193  
|||||

Db 63 CTATTGCTGGAGTCAATGACACTCAAGTTAAAGGCTTTGTTGAAAGAAATGCTGTCATCA 122  
|||||

QY 194 ATGAAGCCCAAAATAGATGAGATCAAGAAATGCAATGTCCAGACACAGCAGAACAGAAAG 253  
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Db 123 ATGAAGCCCAAAATAGATGAGATCAAGAAATGCAATGTCCAGACACAGCAGAACAGAAAG 182  
|||||

QY 254 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATGACACTTGA 313  
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Db 183 TTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAAAGCGTATGACACTTGA 242  
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QY 314 TTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCC 373  
|||||

Db 243 TTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAATTCAGACTATCATCC 302  
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QY 374 TCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAATTCAGAAATGAAATCCAAAGCTTGG 433  
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Db 303 TCAAGGACATTTACTAGTACTGACTCAGAAATTTCAAATTCAGAAATGAAATCCAAAGCTTGG 362  
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QY 434 TC 435  
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Db 363 TC 364  
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GenCore version 5.1.6  
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Perfect score: 435  
Sequence: 1 aagaaagaaggtacagaa.....atgaataccaagcttggtc 435

Scoring table:  
Gapop 10.0 ; Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	433.4	99.6	509	AW994695	AW994695 RC1-BN003
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3	412	94.7	13	BI254532	BI254532 602978522
4	406.4	93.4	809	BF126149	BF126149 601650407
5	394.4	90.7	398	AA180032	AA180032 zo93g12.r
6	383.6	88.2	460	AA293570	AA293570 zt25h11.r

7	370	85.1	676	14	W05802	W05802 za89f05.r1
8	354	81.4	417	10	AV651157	AV651157 AV651157
9	297.8	68.5	395	10	BE070451	BE070451 QV4-BF040
10	286	65.7	305	9	AA860068	AA860068 HGBBT125
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14	172	39.5	461	14	H02935	H02935 yj48b08.r1
15	169.4	38.9	932	9	AL542093	AL542093 AL542093
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17	161	37.0	954	9	AA745982	AA745982 obi18q12.s
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19	147.8	34.0	663	10	AW141748	AW141748 EST291827
20	89.6	20.6	827	9	AJ392468	AJ392468 AJ392468
21	60.6	13.9	646	9	AL542092	AL542092 AL542092
22	53	12.2	963	9	AL566565	AL566565 AL566565
23	47.2	10.9	996	17	CNS00FUH	AL071063 Drosoph11
24	47	10.8	523	13	BJ441951	BJ441951 BJ441951
25	46.4	10.7	642	13	BJ436174	BJ436174 BJ436174
26	46.2	10.6	473	13	BJ379111	BJ379111 BJ379111
27	45	10.3	782	17	AZ175342	AZ175342 SE_0132_A
28	44.8	10.3	584	9	AI231531	AI231531 EST228219
29	44.8	10.3	695	17	AZ318375	AZ318375 IM0037N07
30	44.8	10.3	706	13	BJ345089	BJ345089 BJ345089
31	44.2	10.2	500	13	BJ363187	BJ363187 BJ363187
32	44	10.1	290	14	C90546	C90546 C90546 Dict
33	43.8	10.1	482	13	BJ413360	BJ413360 BJ413360
34	43.8	10.1	528	13	BJ360248	BJ360248 BJ360248
35	43.8	10.1	531	13	BJ389689	BJ389689 BJ389689
36	43.8	10.1	539	13	BJ364065	BJ364065 BJ364065
37	43.8	10.1	559	13	BJ387004	BJ387004 BJ387004
38	43.8	10.1	563	13	BJ324059	BJ324059 BJ324059
39	43.8	10.1	564	13	BJ388447	BJ388447 BJ388447
40	43.8	10.1	567	13	BJ323809	BJ323809 BJ323809
41	43.8	10.1	568	13	BJ391376	BJ391376 BJ391376
42	43.8	10.1	571	13	BJ328095	BJ328095 BJ328095
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION RC1-BN0039-060200-011-a05 BN0039 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AW994695  
VERSION AW994695.1 GI:8254929  
KEYWORDS EST.  
SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 509)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC1-BN0039-060  
 200-011-a05et3-2000-02-06et4-1)  
 Seq primer: puc.18 forward  
 High quality sequence stop: 509.  
 Location/Qualifiers

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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="BN0039"  
 /dev\_stage="Adult"  
 /note="Organ: breast\_normal; Vector: puc18; Site:1: SmaI;  
 Site:2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 205 a 83 C 99 g 122 t

Query Match 99.6%; Score 433.4; DB 10; Length 509;

Best Local Similarity 99.8%; Pred. No. 5.1e-91;

Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 60

DB 17 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 76

QY 61 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120

DB 77 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 136

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 180

DB 137 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 196

QY 181 AAGAAAGGTTCTCAATGAAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 240

DB 197 AAGAAAGGTTCTCAATGAAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 256

QY 241 GCAGACAGAAAGTTCAACTGCTTCTGTAATGTCATCAACTTTCATGAAAGAAAGAGCG 300

DB 257 GCAGACAGAAAGTTCAACTGCTTCTGTAATGTCATCAACTTTCATGAAAGAAAGAGCG 316

QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 360

DB 317 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 376

QY 361 CAGACTATCATCTCAAGGCATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 420

DB 377 CAGACTATCATCTCAAGGCATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 436

QY 421 ATCCAAAGCTTGCTC 435

DB 437 ATCCAAAGCTTGCTC 451

## RESULT 2.

BO051037

LOCUS AGENCOURT\_6954504 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5785846

DEFINITION 5', mRNA sequence.

ACCESSION BO051037

VERSION BQ051037.1 GI:19810377

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1055)

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: cgaos@mail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLML12873 row: j column: 23

High quality sequence stop: 689.

## FEATURES

source

1..1055

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="IMAGE:5785846"

/clone\_lib="NIH\_MGC\_71"

/tissue\_type="leiomyosarcoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site:1: NotI;

Site:2: SalI; Cloned unidirectionally. Primer: Oligo dr.

Average insert size 2.1 kb.

BASE COUNT 352 a 221 c 215 g 267 t

## ORIGIN

Query Match 98.8%; Score 429.8; DB 14; Length 1055;

Best Local Similarity 99.5%; Pred. No. 3.9e-90;

Matches 431; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 60

DB 374 AAGAGAAGGAAGTACAGAAACATGCAGAAACACAGAAAGGAAACCAAGGTTCTCAT 433

QY 61 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120

DB 434 GAATCTCCAACTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 493

QY 121 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 180

DB 494 AAATATATACCACTATTGCTGGAGTCATGACACTAAAGTCAAGTTAAAGGCTTTGTTGCA 553

QY 181 AAGAAAGGTTCTCAATGAAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 240

DB 554 AAGAAAGGTTCTCAATGAAGCCAAATAGATGAGATCAAGATCAATGATGTTCCAGACACA 613

QY 241 GCAGACAGAAAGTTCAACTGCTTCTGTAATGTCATCAACTTTCATGAAAGAAAGAGCG 300

DB 614 GCAGACAGAAAGTTCAACTGCTTCTGTAATGTCATCAACTTTCATGAAAGAAAGAGCG 673

QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 360

DB 674 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTTCAGAGAGAAAT 733

QY 361 CAGACTATCATCTCAAGGCATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 420

DB 734 CAGACTATCATCTCAAGGCATTTACTAGTACTCAGAAATTCAAACTTCAGAAATGAA 793

QY 421 ATCCAAAGCTTGCTG 433

DB 794 ATCCAAAGCTTGCTG 806

## RESULT 3

BI254532

LOCUS 602978522F1 NIH\_MGC\_12 Homo sapiens cDNA clone IMAGE:5123477 5',

DEFINITION mRNA sequence.

ACCESSION BI254532

VERSION BI254532.1 GI:114807044

KEYWORDS EST.

BI254532 776 bp mRNA linear EST 17-JUL-2001

SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
JOURNAL NIH-MGC http://mgc.nci.nih.gov/  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.  
Email: csapb@rmail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM1301 row: 1 column: 06  
High quality sequence stop: 757.

FEATURES  
source  
1. 776  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5123477"  
/clone\_lib="NIH\_MGC\_12"  
/tissue\_type="cervical carcinoma cell line"  
/lab\_host="DH10B"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.4 kb. Library prepared by Life  
Technologies."

BASE COUNT 276 a 136 c 151 g 213 t

ORIGIN  
Query Match 94.7%; Score 412; DB 13; Length 776;  
Best Local Similarity 99.5%; Pred. No. 5.3e-86;  
Matches 434; Conservative 0; Mismatches 0; Indels 2; Gaps 2;  
1 AAGAAAGGAGTACAGAAACATGCGAGAGACAGAGAAAGGAAACCAAGTTCTCAT 60  
102 AAGAAAGGAGTACAGAAACATGCGAGAGACAGAGAAAGGAAACCAAGTTCTCAT 161  
61 GAATCTCCACCTTTAAATCTGAGAGAGTGGCAATTAATTTATCTGATGTTGACTTGAG 119  
162 GAATCTCCACCTTTAAATCTGAGAGAGTGGCAATTAATTTATCTGATGTTGACTTGAG 221  
120 TAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTG 179  
222 TAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTCAAGGCTTTGTTG 280  
180 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGTCAAGTCAAGGCTTTGTTG 239  
281 AAGAATGGTGTCAATGAAGCAAAATAGATGAGATCAAGTCAAGTCAAGGCTTTGTTG 340  
240 AGCAGACAGAAAGTTCACCTGCTTCGTTGATGTCATCACTTCACTGAGAAAGGAGC 299  
341 AGCAGACAGAAAGTTCACCTGCTTCGTTGATGTCATCACTTCACTGAGAAAGGAGC 400  
300 GTATGACACATTTGATTAAGATCTCAAAAAGGCAATCTTTGACTCTTGCAGAGAAAT 359  
401 GTATGACACATTTGATTAAGATCTCAAAAAGGCAATCTTTGACTCTTGCAGAGAAAT 460  
360 TCAGACTATCATCTCAAGGACATTTAGTACTAGAGAAATTCAGAAATTCAGAAATGA 419  
461 TCAGACTATCATCTCAAGGACATTTAGTACTAGAGAAATTCAGAAATTCAGAAATGA 520  
420 AATCCAAGCTTGGTC 435  
521 AATCCAAGCTTGGTC 536

LOCUS BF126149 809 bp mRNA linear EST 24-OCT-2000  
DEFINITION 601650407F1 NIH\_MGC\_76 Homo sapiens cDNA clone IMAGE:3934273 5',  
mRNA sequence.  
ACCESSION BF126149  
VERSION BF126149.1 GI:10965189  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
JOURNAL NIH-MGC http://mgc.nci.nih.gov/  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.  
Email: csapb@rmail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM774 row: n column: 02  
High quality sequence stop: 635.

FEATURES  
source  
1. 809  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3934273"  
/clone\_lib="NIH\_MGC\_76"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site\_1:  
SfiI (ggcgccctcgcc); Site\_2: SfiI (ggcgccattggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCACGCGCGAGCGCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, or T). Average insert size 1.85  
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

BASE COUNT 293 a 127 c 179 g 210 t

ORIGIN  
Query Match 93.4%; Score 406.4; DB 12; Length 809;  
Best Local Similarity 99.3%; Pred. No. 1.1e-84;  
Matches 429; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
1 AAGAAAGGAGTACAGAAACATGCGAGAGACAGAGAAAGGAAACCAAGTTCTCAT 60  
87 AAGAAAGGAGTACAGAAACATGCGAGAGACAGAGAAAGGAAACCAAGTTCTCAT 146  
61 GAATCTCCACCTTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120  
147 GAATCTCCACCTTTAAATCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 206  
121 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 180  
207 AAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCA 265  
181 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACATGTCACAGACACA 240  
266 AAGATGGTGTCAATGAAGCAAAATAGATGAGATCAAGATGACATGTCACAGACACA 325  
241 GCAGAACAGAAAGTTCACTGCTTCGTAATTTGGCATCACTTCAATGGAAGAAAGAGCG 300  
326 GCAGAACAGAAAGTTCACTGCTTCGTAATTTGGCATCACTTCAATGGAAGAAAGAGCG 385  
301 TATGACACATTTGATTAAGATCTCAAAAAGGCAATCTTTGACTCTTTGAGAGAAAT 360  
386 TATGACACATTTGATTAAGATCTCAAAAAGGCAATCTTTGACTCTTTGAGAGAAAT 444

```

361 CAGACTATCATCTCCTCAAGGACATTTACTAGTCTCAGAAATTCAGAAATGAA 420
|||||
445 CAGACTATCATCTCCTCAAGGACATTTACTAGTCTCAGAAATTCAGAAATGAA 504
|||||
421 ATCCAAAGCTTG 432
|||||
505 ATCCAAAGCTGG 516

RESULT 5
AA180032 398 bp mRNA linear EST 31-DEC-1996
LOCUS z093g12.r1 Stratagene ovarian cancer (#937219) Homo sapiens CDNA
DEFINITION clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION AA180032 GI:1761298
VERSION AA180032.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 from Amersham
High quality sequence stop: 263.
Location/Qualifiers
1. 398
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:594502"
/clone_lib="Stratagene ovarian cancer (#937219)"
/sex="female"
/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Cloned unidirectionally. Primer: Oligo dt. Papillary
serous carcinoma, isolated from ascites, 64 year old
caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector;
-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTT 3'"
BASE COUNT 155 a 73 c 73 g 96 t 1 others
ORIGIN

Query Match 90.7%; Score 394.4; DB 9; Length 398;
Best Local Similarity 99.5%; Pred. No. 6,1e-82;
Matches 395; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

32 AGCAGAGAAAGAAACCAAGGTTCTCATGAATCTCCAAACCTTAATCTCTGAACAGTGG 91
|||||
1 AGCAGAGAAAGAAACCAAGGTTCTCATGAATCTCCAAACCTTAATCTCTGAACAGTGG 60
|||||
92 CAATAAATTTACTGATGTTGACTTTCAGTAATATATACCACTATTCTGCGAGTCATCA 151
|||||
61 CAATAAATTTACTGATGTTGACTTTCAGTAATATATACCACTATTCTGCGAGTCATCA 120
|||||
152 CACTAAGTCAAGTTAAAGGCTTTGTTTCGAAAGAAATGGTCTCAATGAAGCCAAATAGATG 211
|||||

```

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121 CACTAAGTCAAGTTAAAGGCTTTGTTTCGAAAGAAATGGTCTCAATGAAGCCAAATAGATG 180
|||||
212 AGATCAAGAAATGACATGTCCTCAAGACACAGACAGAAAGTTCAACTGCTTCGTAATT 271
|||||
181 AGATCAAGAAATGACATGTCCTCAAGACACAGACAGAAAGTTCAACTGCTTCGTAATT 240
|||||
272 GGCATCAACTTTCATGGAAGAAAGCGTATGACACATTTGATTAAGATCTCAAAAAG 331
|||||
241 GGCATCAACTTTCATGGAAGAAAGCGTATGACACATTTGATTAAGATCTCAAAAAG 300
|||||
332 CCAATCTTTTGTACTCTTCGAGAGAAAATTCAGACTATCATCTCTCAAGGACATTACTAGTG 391
|||||
301 CCAATCTTTTGTACTCTTCGAGAGAAAATTCAGACTATCATCTCTCAAGGACATTACTAGTG 360
|||||
392 ACTCAGAAAATTCAAACTTCAGAAATGAAATCCAAAG 428
|||||
361 ACTCGGAAAATTCAAACTTCAGAAATGAAATCCAAAG 397
|||||

RESULT 6
AA293570 460 bp mRNA linear EST 08-AUG-1997
LOCUS zt2sh11.r1 Soares ovary tumor NbHOT Homo sapiens CDNA clone
DEFINITION IMAGE:714213 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN)
); mRNA sequence.
ACCESSION AA293570
VERSION AA293570.1 GI:1941237
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 460)
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL: contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1853 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 125.
Location/Qualifiers
1. 460
/organism="Homo sapiens"
/db_xref="GDB:5934710"
/db_xref="taxon:9606"
/clone="IMAGE:714213"
/clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary; Vector: p77T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5'
TCGTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
FEATURES
Source

```

BASE COUNT 175 a 80 c 81 g 124 t  
ORIGIN

Query Match 88.2%; Score 383.6; DB 9; Length 460;  
Best Local Similarity 99.0%; Pred. No. 2.1e-79;  
Matches 386; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 46 AACCAAGGTTCTCAGTAATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCT 105
DB 1 AACCAAGGTTCTCAGTAATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCT 60
QY 106 GATGTTGACTTCAGTAATAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 165
DB 61 GATGTTGACTTCAGTAATAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTT 120
QY 166 AAAGCGTTTGTTCGAAAGAAATGTTCAATGAAGCCAAATAGATGAGATCAAGAAATGAC 225
DB 121 AAAGCGTTTGTTCGAAAGAAATGTTCAATGAAGCCAAATAGATGAGATCAAGAAATGAC 180
QY 226 ATGTCCAGACAGACAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCAT 285
DB 181 ATGTCCAGACAGACAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCAT 240
QY 286 GGAAGAAAGAGCGCTATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGACT 345
DB 241 GGAAGAAATATATCTGATGACACATTGATTAAGATCTCAAAAAGCCCAATCTTTGACT 300
QY 346 CTTGCAGAGAAATTCAGACTATCATCTCTCAAGGACATTAAGTACTGACATCAAGAAATTC 405
DB 301 CTTGCAGAGAAATTCAGACTATCATCTCTCAAGGACATTAAGTACTGACATCAAGAAATTC 360
QY 406 AACTTCAGAAATGAATCAAAAGCTTGTC 435
DB 361 AACTTCAGAAATGAATCAAAAGCTTGTC 390
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## RESULT 7

W05802 676 bp mRNA linear EST 23-APR-1996  
LOCUS za89f05.r1 Soares\_fetal\_lung\_NbHL19W Homo. sapiens cDNA clone  
DEFINITION IMAGE:299745 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN  
); mRNA sequence.

ACCESSION W05802.1 GI:1278534  
VERSION EST.  
KEYWORDS human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 676)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston  
R., Williamson, A., Woldmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)

## TITLE

JOURNAL Contact: Wilson-RK  
COMMENT Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@wustl.edu  
This clone is available royalty-free through LBNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: mob.REGA+ET

High quality sequence stop: 307.  
Location/Qualifiers  
1..676

## FEATURES

## source

/organism="Homo sapiens"  
/db\_xref="GDB:1244669"  
/db\_xref="taxon:9606"  
/clone="IMAGE:299745"  
/clone\_lib="Soares\_fetal\_lung\_NbHL19W"

/dev\_stage="19 weeks"

/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M. Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NbHL19W."

BASE COUNT 231 a 127 c 138 g 171 t  
ORIGIN

Query Match 85.1%; Score 370; DB 14; Length 676;

Best Local Similarity 98.0%; Pred. No. 3.2e-76;  
Matches 395; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

```
QY 3 GAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCATCA 62
DB 16 GAGAAAGGAAGTACAGAAAACATGCAGAAAGCACAGAAAGGAAACCAAGGTTCTCATCA 75
QY 63 ATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCTGATGTTGACTTCAGTAA 122
DB 76 ATCTCAACCTTAAATCTGAAACAGTGGCAATAATTTATCTGATGTTGACTTCAGTAA 135
QY 123 ATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTT 181
DB 136 ATATATCACCACCTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCG 195
QY 182 AGAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAATGACAAATGCCAAGACACAG 241
DB 196 AGAATGGTGTCAATGAAGCCAAATAGATGAGATGAGATCAAGAATGACAAATGCCAAGAC 255
QY 242 CAGAACAGAAAGTTCACACTGCTT-CGTAAATGGCATCAACTTCATGGAAGAAAGAAAGCG 300
DB 256 CAGAACAGAAAGTTCACACTGCTTCCGTAAATGGCATCAACTTCATGGAAGAAAGAAAGCG 315
QY 301 TATGACACATTCATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTCGACAGAAATTT 360
DB 316 TATGACACATTCATTAAAGATCTCAAAAAGCCCAATCTTTGACTCTTCGACAGAAATTT 375
QY 361 CAGACTATCATCTCAAGGACATTAAGTACTGACTCAGAAAATTT 403
DB 376 CAGACTATCATCTCAAGGACATTAAGTACTGACTCAGAAAATTT 418
```

## RESULT 8

## AV651157

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## COMMENT

AV651157 417 bp mRNA linear EST 15-JAN-2002  
AV651157 GLC Homo sapiens cDNA clone GLC0003 3', mRNA sequence.

AV651157.1 GI:9872171

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 417)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,

Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,

Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,

Hu, G., Gu, J., Chen, Z., and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level

by comparing gene expression profiles of hepatocellular carcinoma

with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

21625106

Contact: Zeguaguan Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

# FEATURES

source  
Location/Qualifiers  
1. 417  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GLCCMD03"  
/clone\_lib="GLC"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"  
BASE COUNT 151 a 74 c 84 g 108 t  
ORIGIN

Query Match .81.4%; Score 354; DB 10; Length 417;  
Best Local Similarity 100.0%; Pred. No. 1.6e-72;  
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 64 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 123  
QY 61 GAATCTCCAACTTAAATCTGAAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 120  
DB 124 GAATCTCCAACTTAAATCTGAAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 183  
QY 121 AAATATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 180  
DB 184 AAATATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 243  
QY 181 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAGACACA 240  
DB 244 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAGACACA 303  
QY 241 GCAGACAGAAAGTTCACCTGCTGTAATGGCATCACTTCTTACTCTTTCAGAG 354  
DB 304 GCAGACAGAAAGTTCACCTGCTGTAATGGCATCACTTCTTACTCTTTCAGAG 363  
QY 301 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTCTTACTCTTTCAGAG 417  
DB 364 TATGACACATGATTAAAGATCTCAAAAAGCCCAATCTTCTTACTCTTTCAGAG 417

RESULT 9  
BE070451/c 395 bp mRNA linear EST 09-JUN-2000  
LOCUS BE070451 QV4-BT0407-020300-122-d09 BT0407 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BE070451  
ACCESSION BE070451  
VERSION BE070451.1 GI:8415097  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and  
Simpson, A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
http://www.ludwig.org.br/scripts/gethtml2.pl?l1=st2-QV4-BT0407-020  
300-122-d09st3-2000-03-02st4-1)  
Seq primer: puc 18 forward  
High quality sequence start: 50  
High quality sequence stop: 395.

FEATURES  
source  
Location/Qualifiers  
1. 395  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="BT0407"  
/dev\_stage="Adult"  
/note="Organ: breast; Vector: puc18; Site\_1: SmaI; Site\_2:  
SmaI; A mini-library was made by cloning products derived  
from ORESTES PCR (U.S. Letters Patent application No. 196  
716 - Ludwig Institute for Cancer Research) profiles  
into the puc 18 vector. Reverse transcription of tissue  
mRNA and cDNA amplification were performed under low  
stringency conditions."  
BASE COUNT 103 a 81 c 67 g 144 t  
ORIGIN

Query Match .68.5%; Score 297.8; DB 10; Length 395;  
Best Local Similarity 95.5%; Pred. No. 2e-59;  
Matches 318; Conservative 0; Mismatches 12; Indels 3; Gaps 1;  
QY 1 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 336 AAGAGAAAGGAGTACAGAAACATGCGAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 277  
QY 61 GAATCTCCAACTTAAATCTGAAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 120  
DB 276 GAATCTCCAACTTAAATCTGAAACAGTGCATTAATTTATCTGATGTTGACTTGAGT 217  
QY 121 AAATATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 180  
DB 216 AAATATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTGCA 157  
QY 181 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAGACACA 240  
DB 156 AAGATGTTGTCATGAGCCAAATAGATGAGATCAAGATGCAATGTCCAGACACA 97  
QY 241 GCAGACAGAAAGTTCACCTGCTGTAATGGCATCACTTCTTACTCTTTCAGAG 297  
DB 96 GCAGACAGAAAGTTCACCTGCTGTAATGGCATCACTTCTTACTCTTTCAGAG 37  
QY 298 GCGTATGACACATGATTAAAGATCTCAAAAAA 330  
DB 36 TAGTATGACACATGATTAAAGATCTCAATAA 4

RESULT 10  
AA860068 305 bp mRNA linear EST 11-MAR-1998  
LOCUS HGBBT125 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.  
DEFINITION AA860068  
ACCESSION AA860068  
VERSION AA860068.1 GI:2952547  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 305)  
AUTHORS Jin, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.Q.  
TITLE DDRT-PCR of Human Glioblastoma Cell Line BT-325 cDNAs  
JOURNAL Unpublished (1997)



## COMMENT

Contact: Boqin Qiang  
National Laboratory of Medical Molecular Biology, CAMS & PUMC  
Institute of Basic Medical Sciences, Peking Union Medical College &  
Chinese Academy of Medical Sciences  
5 Dong San Tiao, Beijing 100005, P.R. China  
Tel: (010)65296411  
Fax: 8610-5240529  
Email: zh357@iname.com

Seq primer: M13 Reverse Primer.

## FEATURES

source

## FEATURES

source

Location/Qualifiers  
1..1152  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5755724"  
/clone\_lib="NIH\_MGC\_118"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV.  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

BASE COUNT 122 a 52 c 64 g 67 t  
ORIGIN

Query Match 65.7%; Score 286; DB 9; Length 305;  
Best Local Similarity 100.0%; Pred. No. 1.1e-56;  
Matches 286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 20 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 79  
QY 61 GAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 120  
DB 80 GAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 139  
QY 121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 180  
DB 140 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 199  
QY 181 AAGATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 200 AAGATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 259  
QY 241 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATG 286  
DB 260 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATG 305

## RESULT 11

BM922638

LOCUS

DEFINITION AGENCOURT\_6652776 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5755724  
5', mRNA sequence.

ACCESSION BM922638

VERSION 1

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 305)  
NIH-MGC <http://www.ncbi.nlm.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished 1999  
Contact: Robert Strausberg, Ph.D.  
Email: cgaab3@fmail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LLAM12795 row: c column: 21

High quality sequence start: 52

High quality sequence stop: 628.

## FEATURES

source

Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:5755724"  
/clone\_lib="NIH\_MGC\_118"  
/tissue\_type="leukocyte"  
/lab\_host="DH10B"  
/note="Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: EcoRV.  
(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."

BASE COUNT 354 a 273 c 276 g 249 t  
ORIGIN

Query Match 60.7%; Score 264.2; DB 14;  
Best Local Similarity 91.3%; Pred. No. 1.6e-51;  
Matches 337; Conservative 0; Mismatches 23; Indels 9; Gaps 5;

QY 1 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
DB 470 AAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 529  
QY 61 GAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 120  
DB 530 GAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGT 589  
QY 121 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 180  
DB 590 AAATATATCACCACTATTGCTGGAGTCATGACACTAAGTAAAGGCTTTGTTGCA 649  
QY 181 AAGATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 650 AAGATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGAT 709  
QY 241 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATG 295  
DB 710 GCAGAACAGAAAGTTCACCTGCTTCTGTAATTTGGCATCAACTTCATG 769  
QY 296 AAGCGTATGACACATT-GATTAAGATCTCAAAAAA---GCCAATCTTTGTACTTTGCA 351  
DB 770 AAGCGTATGACACATTGATTAAGATCTCAAAAAAAGCCCAACCCCTTGGACCTCTGCG 829  
QY 352 GAGAAATTT 360  
DB 830 AAGAAATTT 838

## RESULT 12

AV715411

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 696)

Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,

AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence.

AV715411

AV715411

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 696)

Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,

Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,

Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z. and Han, Z.  
 Homo sapiens cDNA DCB clones  
 Unpublished (2000)  
 Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shouying Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P.R. China  
 Tel: 86-21-50801919 (ex. 45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn  
 This clone is available at CHGC in Shanghai.

Location/Qualifiers

## FEATURES

source

1. .696  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="DCBAUC01"  
 /clone\_lib="DCB"  
 /cell\_type="dendritic cells"  
 /dev\_stage="mature"  
 /lab\_host="BM25.8"  
 /note="Vector: pTriplex2; Site\_1: sfIIA; Site\_2: sfIIB"  
 210 a 141 c 156 g 189 t

BASE COUNT 210 a 141 c 156 g 189 t  
 ORIGIN  
 Query Match 46.3%; Score 201.2; DB 10; Length 696;  
 Best Local Similarity 98.5%; Pred. No. 7.3e-37;  
 Matches 203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 1 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
 Db 478 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 537  
 Oy 61 GAATCTCAACCTTAAATCCTGGAACAGTGCATCAATTAATTTATCTGATGTTGACTTGTAGT 120  
 Db 538 GAATCTCAACCTTAAATCCTGGAACAGTGCATCAATTAATTTATCTGATGTTGACTTGTAGT 597  
 Oy 121 AAATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 180  
 Db 598 AAATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 657  
 Oy 181 AAGAATGGTGTCAATGAAGCCAAAT 206  
 Db 658 AAGAATGGTGTCAATGAAGCCAACT 683

RESULT 13  
 AA852070  
 LOCUS  
 DEFINITION HGBBT116 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.  
 AA852070  
 ACCESSION  
 VERSION AA852070.1 GI:2939608  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 217)  
 Jia, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.Q.  
 DORT-PCR of Human Glioblastoma Cell Line BT-325 cDNAs  
 Unpublished (1997)  
 Contact: Boqin Qiang  
 National Laboratory of Medical Molecular Biology, CAMS & PUMC  
 Institute of Basic Medical Sciences, Peking Union Medical College &  
 Chinese Academy of Medical Sciences  
 5 Dong Dan San Tiao, Beijing 100005, P.R. China  
 Tel: (010) 65296411  
 Fax: 8610-5240529  
 Email: zh357@iname.com  
 Seq primer: M13 Reverse Primer.  
 Location/Qualifiers  
 1. .217  
 /organism="Homo sapiens"

## FEATURES

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/db\_xref="taxon:9606"  
 /clone\_lib="Human Glioblastoma Cell"  
 /cell\_type="Glioblastoma Cell"  
 /cell\_line="BT-325"  
 /lab\_host="E.coli DH5a"  
 /note="Organ: Brain; Vector: PCR11, Invitrogen; Total RNA  
 was isolated from human glioblastoma cell line BT325.  
 Then Differential Display RT-PCR was conducted between  
 normal and all-trans Retinoic Acid induced cell.  
 Differentially expressed PCR products were cloned and  
 sequenced."  
 86 a 34 c 48 g 49 t  
 BASE COUNT 86 a 34 c 48 g 49 t  
 ORIGIN  
 Query Match 45.1%; Score 196.4; DB 9; Length 217;  
 Best Local Similarity 99.5%; Pred. No. 8.2e-36;  
 Matches 197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 60  
 Db 20 AAGAGAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGGTTCTCAT 79  
 Oy 61 GAATCTCAACCTTAAATCCTGGAACAGTGCATCAATTAATTTATCTGATGTTGACTTGTAGT 120  
 Db 80 GAATCTCAACCTTAAATCCTGGAACAGTGCATCAATTAATTTATCTGATGTTGACTTGTAGT 139  
 Oy 121 AAATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 180  
 Db 140 AAATATATCACCACCTATTTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTTCTGA 199  
 Oy 181 AAGAATGGTGTCAATGAA 198  
 Db 200 AAGAATGGTGTCAATGAA 217  
 RESULT 14  
 H02935  
 LOCUS  
 DEFINITION Y146B08.r1 Soares placenta NB2HP Homo sapiens cDNA clone  
 IMAGE:151767 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR (HUMAN  
 );, mRNA sequence.  
 H02935  
 ACCESSION  
 VERSION H02935.1 GI:865868  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 461)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
 M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,  
 Rifkin, L., Rohlfsing, T., Soares, M., Tan, F., Trevas, E., Waterston  
 R., Williamson, A., Wohldmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1432  
 High quality sequence stops: 316  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert Length: 1432 Std Error: 0.00  
 Seq primer: M13RP1  
 High quality sequence stop: 316.  
 Location/Qualifiers  
 1. .461  
 /organism="Homo sapiens"  
 /db\_xref="GDB:563902"

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/db_xref="taxon:9606"
/clone="IMAGE:151767"
/clone_lib="Soares placenta Nb2HP"
/sex="female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AAGTGAAGAATTCGGCGCGCAGGAATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaudo.
2 others
BASE COUNT      145 a      76 c      96 g      142 t
ORIGIN

Query Match      39.5%; Score 172; DB 14; Length 461;
Best Local Similarity 100.0%; Pred. No. 4.4e-30;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      264 TCCTAATGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTGATTAAGATCT 323
Db      1 TCCTAATGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTGATTAAGATCT 60

QY      324 CAAAAAGCCAACTTTGTACTCTTCGAGAGAAATTCAGACTATCATCTCAAGGACAT 383
Db      61 CAAAAAGCCAACTTTGTACTCTTCGAGAGAAATTCAGACTATCATCTCAAGGACAT 120

QY      384 TACTAGTACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGTC 435
Db      121 TACTAGTACTCAGAAATTCAAACTTCAGAAATGAAATCCAAAGCTTGTC 172

RESULT 15
AL542093
LOCUS      AL542093 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE009YI06 5 prime
DEFINITION      , mRNA sequence.
ACCESSION      AL542093
VERSION        AL542093.1 GI:12873796
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 932)
AUTHORS        Li, W. B., Gruber, C., Jessee, J., and Polayes, D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished (2001)
COMMENT        Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES       Location/Qualifiers
source         1..932
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="CS0DE009YI06"
               /clone_lib="LTI_FL002_PL1"
               /lab_host="DH10B"
               /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
technologies. Contact : feng liang life technologies, a
division of invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      270 a      210 c      233 g      218 t      1 others

```

## ORIGIN

```

Query Match      38.9%; Score 169.4; DB 9; Length 932;
Best Local Similarity 98.3%; Pred. No. 2e-29;
Matches 170; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AACAGAAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGCAAAACCAAGCTTCTCAT 60
Db      753 AAGAGAAAGGAAGTACAGAAACATGCAGAAAGCAGACAGAAAGCAAAACCAAGCTTCTCAT 812

QY      61 GAATCTCCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 120
Db      813 GAATCTCCCAACCTTAAATCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGT 872

QY      121 AAATATATCACCACACTATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCTT 173
Db      873 AAATATATCACCACACTATTTGCTGGAGTCATGACACTAAGTCAAGTTAAAGCTT 925

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Search completed: June 15, 2003, 21:11:49  
Job time : 1428 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 21:13:09 ; Search time 1535 Seconds  
(without alignments)  
2749.125 Million cell updates/sec

Title: US-09-884-987-2\_COPY\_175\_319

Perfect score: 750

Sequence: 1 GWLCLLLPIPLVWVRKE.....KANLCTLAETIILKDKIT 145

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LISP=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09884987 -CGEN\_1\_1\_1319=runat\_09062003\_140300\_13176 -NCPU=6 -ICPU=3  
-NO\_MMMap -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*

29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
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41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	750	100.0	761	9	HSPASCD52	247994 H.sapiens F
2	750	100.0	899	9	HSPAS4DEL	270519 H.sapiens F
3	750	100.0	920	9	HSPAS34	X83490 H.sapiens m
4	750	100.0	1008	6	E05336	E05336 DNA encodin
5	750	100.0	1457	6	E35160	E35160 Method for
6	750	100.0	2534	6	A87646	A87646 Sequence 4
7	750	100.0	2534	6	AR163572	AR163572 Sequence
8	750	100.0	2534	6	AR173438	AR173438 Sequence
9	750	100.0	2534	6	E05110	E05110 CDNA encodi
10	750	100.0	2534	6	E09121	E09121 CDNA encodi
11	750	100.0	2534	6	HUMFASANT	M67454 Human Fas a
12	750	100.0	2551	6	AR143111	AR143111 Sequence
13	750	100.0	2551	9	HSAP01	X63717 H.sapiens m
14	750	100.0	2719	9	BC012479	BC012479 Homo sapi
15	750	100.0	8282	6	AX146813	AX146813 Sequence
16	750	100.0	8345	6	AX146814	AX146814 Sequence
17	743	99.1	3009	6	AX060340	AX060340 Sequence
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19	726	96.8	1468	6	AX060336	AX060336 Sequence
20	681	90.8	983	9	HSPASAP0A	266556 H.sapiens F
21	670	89.3	1483	6	AX060338	AX060338 Sequence
22	663	88.4	836	9	HSPASCD53	247995 H.sapiens F
23	663	88.4	836	9	HSPAS4DEL	270520 H.sapiens F
24	663	88.4	857	9	HSPAS346	X83491 H.sapiens F
25	663	88.4	945	9	HSPASCD51	247993 H.sapiens F
26	663	88.4	1104	9	HSPAS6	X83493 H.sapiens m
27	663	88.4	2471	6	I58632	I58632 Sequence 18
28	663	88.4	2471	6	I63530	I63530 Sequence 18
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31	577	76.9	1068	9	AF326208	AF326208 Macaca as
32	569	75.9	1361	9	AF344843	AF344843 Carcoebu
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39	531	70.8	1005	9	AF332357	AF332357 Macaca ar
40	479	63.9	1840	9	HSAPT9	X81342 H.sapiens A
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ALIGNMENTS

RESULT 1

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Query Match:	100.00%	Indels:	0



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Qy	21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40 
Dd	777 GTACAGAACAATCGCAGAAAGCACAGAAAGGAAGAACCAAGGTTCTCATGAATCTCCAACC 836 
Qy	41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValaspLeuSerLysTyrlleThr 60 
Dd	837 TTAATCCTCGAAGACAGTGGCAATAAAATTTATCTGATCTTGACTTGACTGAATAATATATCACC 896 
Qy	61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80 
Dd	897 ACTATTGCTGGAGTCATGCACATAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAGATGGTGTC 956 
Qy	81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100 
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Qy	121 IleLysAspLeuLysLysAlaAsnLeuCystThrLeuAlaGluLysIleGlnThrIleIle 140 
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Dd	1137 CTCAGGACATTACT 1151 
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LOCUS	Human Fas antigen (fas) mRNA, complete cds.
DEFINITION	M67454
ACCESSION	M67454.1 GI:182409
VERSION	Fas antigen; cell surface antigen; transmembrane protein.
KEYWORDS	Homo sapiens (clone pf58) (tissue library: pCEV4) CDNA to mRNA.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 2534): Itoh,N., Yonehara,S., Ishii,A., Yonehara,M. Mizushima,S., Sameshima,M., Hase,A., Seto,Y. and Nagase,S. The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis Cell 66 (2), 233-243 (1991) J91309137
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	

July 1991

LOCUS	HSAP01	2551 bp	mRNA	linear	PRI 19-JUL-1996
DEFINITION	H.sapiens mRNA for APO-1 cell surface antigen.				
ACCESSION	X63717				

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VERSION      X63717.1 GI:28741
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SOURCE      Homo sapiens.
ORGANISM     Homo sapiens
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AUTHORS     Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TITLE       1 (bases 1 to 2551)
JOURNAL     Kramer, P.H.
REFERENCE    Direct Submission
            Submitted (10-FEB-1992) P.H. Kramer, German Cancer Research
            Center, Tumor Immunology Program, Im Neuenheimer Feld 280, 6900
            Heidelberg, FRG
REFERENCE    2 (bases 1 to 2551)
AUTHORS     Oehm, A., Behrmann, I., Falk, W., Pawlita, M., Maier, G., Li-Weber, M.,
            Richards, S., Dhein, J., Trauth, B.C., Postings, H. and Kramer, P.H.
TITLE       Purification and molecular cloning of the APO-1 cell surface
            antigen, a member of the tumor necrosis factor/nerve growth factor
            receptor superfamily. Sequence identity with the Fas antigen
            J. Biol. Chem. 267 (15), 10709-10715 (1992)
JOURNAL     92268122
MEDLINE     1375228
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DEFINITION Homo sapiens, Similar to tumor necrosis factor receptor
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            complete cds.
ACCESSION  BC012479
VERSION     BC012479.1 GI:15214691
KEYWORDS    MGC.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
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AUTHORS     Strausberg, R.
TITLE       Direct Submission
JOURNAL     Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT      Contact: MGC help desk
            Email: cgapsb-re@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: villalona@bcm.tmc.edu.
            Villalona, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
            A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
            Muzny, D.M., Gibbs, R.A.
            Clone distribution: MGC clone distribution information can be found
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Rigel Pharmaceuticals, Inc. (US)  
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VERSION AX146813.1 GI:14285162  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 8282)  
AUTHORS Kinshia,T.M.  
TITLE Methods and compositions for screening using diphtheria toxin constructs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: June 15, 2003, 21:11:59 ; Search time 217 Seconds  
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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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- 22: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.\*
- 23: /SID52/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*
- 24: /SID52/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	750	100.0	920	17	AAT34529	Human Fas soluble
2	750	100.0	920	24	ABK84693	Human cDNA differe
3	750	100.0	1167	17	AAT34526	Human Fas antigen
4	750	100.0	1457	21	AAA39167	Apocobody3sc fusi
5	750	100.0	2534	13	AAQ29959	Human cell surface
6	750	100.0	2534	16	AAQ95297	Plasmid pF58 contg
7	750	100.0	2534	17	AAT16303	hFas coding sequen
8	750	100.0	2534	18	AAV07002	Human Fas antigen
9	750	100.0	2534	19	AAV32993	Fas cDNA. Mammali
10	750	100.0	2551	21	AAAC61798	DNA encoding a hum
11	750	100.0	2551	24	ABN79588	Human Fas locus HS
12	750	100.0	8282	21	AAZ34938	C12ScFas survival
13	750	100.0	8282	22	AAF30947	C12ScFas survival
14	750	100.0	8345	21	AAZ34939	Abhhh survival con
15	750	100.0	8345	22	AAF30948	Abhhh survival con
16	743	99.1	3009	22	AAA91131	Fit-lextraFas/cy
17	743	99.1	3009	22	AAA91132	Flk-lextraFas/cy
18	726	96.8	1468	22	AAA91129	CD44hextraFas/cy
19	670	89.3	1483	22	AAA91130	CD44hextra/cmfascy
20	663	88.4	836	24	ABN79685	Sequence #9 used t
21	663	88.4	1104	17	AAT34527	Human Fas soluble
22	663	88.4	2471	16	AAQ93879	Fas-delta-TM cDNA.
23	663	88.4	2471	20	AAQ24878	Soluble Fas recept
24	658	87.7	857	17	AAT34530	Human Fas soluble
25	601	80.1	398	24	ABL79512	Human ovarian can
26	566	75.5	460	24	ABL80178	Human ovarian can
27	554.5	73.9	975	17	AAT34528	Human Fas soluble
28	554.5	73.9	975	24	ABL63728	Breast cancer rela
29	554.5	73.9	975	24	ABL68887	Kidney cancer rela
30	465	62.0	1840	24	ABN79684	Sequence #8 used t
31	314.5	41.9	984	14	AAQ48008	Murine Fas gene.
32	314.5	41.9	1480	21	AAAC61859	DNA encoding a mur
33	314.5	41.9	1480	24	ABN79649	Mouse fas locus MU
34	314.5	41.9	1506	16	AAQ95302	Murine Fas antigen
35	314.5	41.9	1506	17	AAT16305	Coding sequence fo
36	314.5	41.9	1506	20	AAV71961	Fas ligand (FasL)
37	153	20.4	338	24	ABN79682	Sequence #6 used t
38	111	14.8	80	21	AAA39161	Human Fas antigen
39	101	13.5	60	24	ABN40425	Human spliced tran
40	101	13.5	60	24	ABN56760	Human spliced tran
41	101	13.5	60	24	ABN58963	Fas antigen antise
42	99.5	13.3	257	17	AAT34538	Human spliced tran
43	93	12.4	60	24	ABN58759	Human spliced tran
44	89	11.9	855	24	ABN79681	Sequence #5 used t
45	86	11.5	15923	24	ABL70179	Chemically treated

ALIGNMENTS

RESULT 1

AAT34529

ID AAT34529 standard; cDNA; 920 BP.

XX

AC AAT34529;

XX

XT 10-OCT-1996 (first entry)

XX

DE Human Fas soluble antigen Fas del3 cDNA.

XX

DE Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;

KW angioimmunoblastic lymphadenopathy; AILD; SS.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 26..307

FT /\*tag= a









PT DNA encoding human cell surface antigen - used to clarify  
 PT apoptosis mechanism of various types of cell, and to prepare  
 PT monoclonal antibodies that react with tumour cells expressing Fas

XX Claim 3; Fig 1 and 2; 27pp; English.

XX A cDNA library was prepared from polyA+ RNA from the human lymphoma  
 CC cell line KT-3. The cDNA was ligated to BstXI-cut vector pCEV4 via  
 CC BstXI linkers. The KT3 cDNA library was used to transfect monkey COS-  
 CC 7 cells which were then suspended in buffer containing murine anti-Fas  
 CC Ab. The cells were "panned" on plates pre-coated with goat anti-mouse  
 CC antibodies. The Fas-expressing cells adhered to the plates.  
 CC Extrachromosomal DNA was prepared from adhered cells and used to  
 CC transform E. coli VM100 cells. A 520bp XhoI-BamHI fragment from a  
 CC positive clone (pF3) was used to screen the KT-3 cDNA library. The  
 CC longest cDNA clone was designated pF58 and contains an ORF corresp.  
 CC to a 335 amino acid pre-protein and a 319 amino acid mature protein  
 CC (i.e. human Fas antigen).

XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

#### Alignment Scores:

Pred. No.: 8,9e-83 Length: 2534  
 Score: 750.00 Matches: 145  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAQ29959 (1-2534)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
 DB 717 GGGTGGCTTGTCTCTCTTTTGGCCAAATCCACTTAATTTGGGTGAAGAGAAAGAA 776  
 QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
 DB 777 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 836  
 QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60  
 DB 837 TTAATTCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACCC 896  
 QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
 DB 897 ACTATTGCTGGAGTCATGACACATGAATCAAGTTAAAGGCTTTGTCGAAAGAAATGGTGTC 956  
 QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
 DB 957 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCACAGACACAGCAGAAAGAA 1016  
 QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120  
 DB 1017 GTTCAACTGCTTCTGTAATTTGGCATCACTTCAATGGAAGAAAGAAAGCGTATGACATTG 1076  
 QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140  
 DB 1077 ATTAAGATCTCAAAAGCCAAATCTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 1136  
 QY 141 LeuLysAspIleThr 145  
 DB 1137 CTCAAGGACATTACT 1151

#### RESULT 6

AAQ95297  
 ID AAQ95297 standard; cDNA; 2534 BP.

XX AC AAQ95297;  
 XX DT 19-FEB-1996 (first entry)  
 XX DE Plasmid pF58 contg. human Fas cDNA.  
 XX

KW Plasmid pF58; human Fas cDNA; soluble membrane protein;  
 KW antibody production; diseases; treatment; prevention; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 195..1202

XX sig\_peptide /\*tag= a

XX mat\_peptide /\*tag= b

XX JF07115988-A.

XX 09-MAY-1995.

XX 26-OCT-1993; 93JP-0267644.

XX 26-OCT-1993; 93JP-0267644.

XX (NIBS) JAPAN TOBACCO INC.

XX WPI; 1995-202847/27.

XX P-PSDB; AAR78606.

XX Preparation of soluble membrane proteins - for their use in antibody

XX production for the treatment and prevention of related diseases

XX Example 1; Pages 15-17; 51pp; Japanese.

XX AAQ95297 is the plasmid pF58 which contains the human Fas cDNA. The

XX plasmid was used in the construction of an expression vector for

XX the prodn. of recombinant soluble membrane proteins. The proteins

XX can be used in antibody prodn. for the treatment and prevention of

XX related diseases.

XX Sequence 2534 BP; 817 A; 487 C; 503 G; 727 T; 0 other;

XX Alignment Scores:

Pred. No.: 8,9e-83 Length: 2534

Score: 750.00 Matches: 145

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 16 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAQ95297 (1-2534)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20

DB 717 GGGTGGCTTGTCTCTCTTTTGGCCAAATCCACTTAATTTGGGTGAAGAGAAAGAA 776

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40

DB 777 GTACAGAAACATGCAGAAAGCAGACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 836

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60

DB 837 TTAATTCCTGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACCC 896

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80

DB 897 ACTATTGCTGGAGTCATGACACATGAATCAAGTTAAAGGCTTTGTCGAAAGAAATGGTGTC 956

QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100

DB 957 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCACAGACACAGCAGAAAGAA 1016

QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120

DB 1017 GTTCAACTGCTTCTGTAATTTGGCATCACTTCAATGGAAGAAAGAAAGCGTATGACATTG 1076





```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAV32993 (1-2534)

QY 1 GlyTrrLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 717 GGGTGGCTTGTCTCTCTTTGGCAATTCACATAATGTTGGTGAAGAGAAAGGAA 776

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 777 GTACAGAAACATGTCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 836

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60
DB 837 TTAATCTGTAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATATCACC 896

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTCT 956

QY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 957 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGACAGAA 1016

QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrsphrLeu 120
DB 1017 GTCAACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAAAGCGTATCAGCATTC 1076

QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
DB 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136

QY 141 LeuLysAspIleThr 145
DB 1137 CTCAGGACATTACT 1151

RESULT 10
AAC61798
ID AAC61798 standard; DNA; 2551 BP.
XX
AC AAC61798;
XX
DT 06-MAR-2001 (first entry)
XX
DE DNA encoding a human Fas (Apo-1) protein.
XX
KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fap-1; hepatitis;
KW Fas associated protein 1; protein tyrosine phosphatase; cancer;
KW autoimmune disease; inflammatory disease; lymphoma; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 221..1228
FT /tag- a "Fas"
FT /product- "Fas"
XX
XX WO200061150-A1.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09540.
XX
XX 12-APR-1999; 99US-0290640.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM, Marcusson EG;
XX
XX WPI; 2000-628395/60.
XX
XX P-PSDB; AAB19341.
XX

XX Antisense oligonucleotides for treating hepatitis and colon, liver or
PT lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein
PT 1 (Fap-1) expression
XX
PS Example 2; Page 71-73; 116pp; English.
XX
CC The present sequence encodes human Fas (Apo-1). The specification
CC describes antisense compounds which are targeted to the 5'-untranslated
CC region, translational start site, translational termination region
CC or 3'-untranslated region of nucleic acid molecules encoding Fas, Fas
CC ligand (FasL), or Fap-1 (Fas associated protein 1, protein tyrosine
CC phosphatase). The antisense compounds are used to inhibit the
CC expression of Fas, FasL or Fap-1 in cells or tissues. They are used
CC to treat autoimmune or inflammatory diseases such as hepatitis. They
CC can also be used to treat cancer, especially colon, liver or lung
CC cancer or lymphoma.
XX
SQ Sequence 2551 BP; 826 A; 493 C; 508 G; 724 T; 0 other;

Alignment Scores:
Pred. No.: 8,99e-83 Length: 2551
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AAC61798 (1-2551)

QY 1 GlyTrrLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 743 GGGTGGCTTGTCTCTCTTTGGCAATTCACATAATGTTGGTGAAGAGAAAGGAA 802

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 803 GTACAGAAACATGTCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 862

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60
DB 863 TTAATCTGTAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATATCACC 922

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 923 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGGAAGAAATGGTGTCT 982

QY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 983 AATGAAGCCAAAATAGATGAGATCAAGAATGACAATGTCCAAGACACAGACAGAA 1042

QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrsphrLeu 120
DB 1043 GTCAACCTGCTTCGTAATTTGGCATCAACTTTCATGGAAGAAAGAAAGCGTATCAGCATTC 1102

QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140
DB 1103 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1162

QY 141 LeuLysAspIleThr 145
DB 1163 CTCAGGACATTACT 1177

RESULT 11
ABN79588
ID ABN79588 standard; DNA; 2551 BP.
XX
AC ABN79588;
XX
DT 29-JUL-2002 (first entry)
XX
DE Human Fas locus HSAPO1.
XX
XX Human; immunosuppressive; antiinflammatory; hepatotropic;
```



CC then induced with IL-4 or IL-13, and the presence or absence of the  
CC reporter gene is detected. Absence of the reporter gene indicates  
CC that the agent inhibits the promoter.

XX  
SQ Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;

Alignment Scores:  
Pred. No.: 4.63e-82 Length: 8282  
Score: 750.00 Matches: 145  
Percent Similarity: 100.00% Conservatism: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAZ34938 (1-8282)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProileProleuLeuValTrpValVallysArgLysGlu 20  
DB 4401 GGTTGGCTTTGCTCTCTCTTTGCCAATTCACATAATTTGGGTGAAGAGAAAGAA 4342  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
DB 4341 GTACAGAAACATGTCAGAACGACAGAGAAAGAAACCAAGGTTCTCATGATCTCCAAAC 4282  
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60  
DB 4281 TTAATCTCTGAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAAATATATACAC 4222  
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
DB 4221 ACTATTGCTGGAGTCATGACACTAAAGTCAAGTAAAGGCTTTGTTGCAAGAAATGGTGT 4162  
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
DB 4161 AATGAACCAAAATAGATGAGATCAAGAAATGACATGTCACAGACAGACAGACAGAA 4102  
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120  
DB 4101 GTTCAACTGCTTGTAAATTTGGCATCACTTTCATGGAAGAAAGAGCGGTATGACACATTG 4042  
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140  
DB 4041 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 3982  
QY 141 LeuLysAspIleThr 145  
DB 3981 CTCAAGGACATTACT 3967

## RESULT 13

AAF30947/C  
ID AAF30947 standard; DNA; 8282 BP.

XX  
AC AAF30947;

XX 23-JUL-2001 (first entry)

XX C12ScFas survival construct.

XX Interleukin-4 inducible epsilon promoter; human; IgE; antibody;  
KW immunoglobulin E; allergy; therapy; switch rearrangement; vector;  
KW Fas; survival construct; death gene; ds.

XX Chimeric - Unidentified.

XX W0200134806-A2.

XX 17-MAY-2001.

XX 13-NOV-2000; 2000WO-US31232.

XX 12-NOV-1999; 99US-0165189.

XX (RIGE-) RIGEL PHARM INC.

XX Kinsella TM;  
PI  
XX  
DR WPI; 2001-335931/35.  
XX

PT Screening for agents capable of inhibiting a promoter, especially  
PT interleukin-4 inducible epsilon promoter involved in immunoglobulin E  
PT production, by using diphtheria toxin constructs -

PS Disclosure; Fig 12A-C; 80pp; English.

XX The present sequence is that of survival construct C12ScFas in  
CC which the interleukin-4 inducible epsilon promoter-chimeric  
CC Fas(CD95)-internal ribosome entry site-hygroycin-bovine growth  
CC hormone polyA tail is placed in the C12s vector backwards so that  
CC no leaky transcription occurs through the CMV promoter. Methods of  
CC the invention utilize diphtheria toxin for screening purposes,  
CC especially for identifying modulators of IgE synthesis, secretion  
CC and switch rearrangement. A claimed method of screening for  
CC bioactive agents capable of inhibiting the IL-4 inducible epsilon  
CC promoter (see AAF30941), which is involved in IgE switching,  
CC comprises: combining a candidate bioactive agent and a cell that  
CC does not endogenously express heparin-binding epidermal growth  
CC factor-like growth factor (HBEGF) and which comprises a fusion  
CC nucleic acid encoding HBEGF; inducing the promoter with IL-4;  
CC adding diphtheria toxin to the cell; and determining whether the  
CC cell is dead. Survival constructs carrying a death gene and a  
CC drug selectable marker have been used to generate an epsilon  
CC promoter survival cell line. Inhibitors of IgE synthesis can be  
CC identified that prevent the production of IgE and reduce or  
CC eliminate an allergic response.

XX SQ Sequence 8282 BP; 1892 A; 2249 C; 2040 G; 2101 T; 0 other;

## Alignment Scores:

Pred. No.: 4.63e-82 Length: 8282  
Score: 750.00 Matches: 145  
Percent Similarity: 100.00% Conservatism: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAF30947 (1-8282)

QY 1 GlyTrpLeuCysLeuLeuLeuProileProleuLeuValTrpValVallysArgLysGlu 20  
DB 4401 GGTTGGCTTTGCTCTCTCTTTGCCAATTCACATAATTTGGGTGAAGAGAAAGAA 4342  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
DB 4341 GTACAGAAACATGTCAGAACGACAGAGAAAGAAACCAAGGTTCTCATGATCTCCAAAC 4282  
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60  
DB 4281 TTAATCTCTGAACAGTGGCAATAATTTATCTGATCTTGACCTGAGTAAATATATACAC 4222  
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
DB 4221 ACTATTGCTGGAGTCATGACACTAAAGTCAAGTAAAGGCTTTGTTGCAAGAAATGGTGT 4162  
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
DB 4161 AATGAACCAAAATAGATGAGATCAAGAAATGACATGTCACAGACAGACAGACAGAA 4102  
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120  
DB 4101 GTTCAACTGCTTGTAAATTTGGCATCACTTTCATGGAAGAAAGAGCGGTATGACACATTG 4042  
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140  
DB 4041 ATTAAGATCTCAAAAAGCAATCTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 3982



Qy	1	Gly	Trp	Leu	Cys	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Val	Trp	Val	Lys	Arg	Lys	Glu	20
Db	4401	GGG	TGG	CTT	GTC	TTT	CTT	TTT	TTC	AAAT	TCC	AAAT	TGT	TTT	GGG	TGA	AGAG	AAAG	AA	4342

CC bioactive agents capable of inhibiting the IL-4 inducible epsilon  
CC promoter (see AAF30941), which is involved in IgE switching,  
CC comprises: combining a candidate bioactive agent and a cell that  
CC does not endogenously express heparin-binding epidermal growth  
CC factor-like growth factor (HBEGF) and which comprises a fusion  
CC nucleic acid comprising the IL-4 inducible epsilon promoter and a  
CC nucleic acid encoding HBEGF; inducing the promoter with IL-4;  
CC adding diphtheria toxin to the cell; and determining whether the  
CC cell is dead. Survival constructs carrying a death gene and a  
CC drug selectable marker have been used to generate an epsilon  
CC promoter survival cell line. Inhibitors of IgE synthesis can be  
CC identified that prevent the production of IgE and reduce or  
CC eliminate an allergic response.

XX

SQ Sequence 8345 BP; 1915 A; 2264 C; 2084 G; 2082 T; 0 other;

## Alignment Scores:

Pred. No.:	4.68e-82	Length:	8345
Score:	750.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAF30948 (1-8345)

QY	1	GlyTyrLeuCysLeuLeuLeuLeuProIleValTrpValLysArgLysGlu	20
Db	4401	GGGTGGCTTGTCTCTCTTTGCCAATCCACTAATTTGTTGGTGAAGAGAAAGGAA	4342
QY	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40
Db	4341	GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCCCAACC	4282
QY	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr	60
Db	4281	TTAAATCCCTGAACACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACCC	4222
QY	61	ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal	80
Db	4221	ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTTGGAAGAAGTGGTGC	4162
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValIcInAspThrAlaGluGlnLys	100
Db	4161	ANTGAGCCCAATAGATGAGATCAGATGACATGACATGTCACAGACACACACAGAGAA	4102
QY	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeu	120
Db	4101	GTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTG	4042
QY	121	IleLysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
Db	4041	ATTAAGATCTCAAAAGACCAATCTTTGTACTCTTGACAGAGAAATTCAGACTATCATC	3982
QY	141	LeuLysAspIleThr	145
Db	3981	CTCAGGACATTAAT	3967

Search completed: June 15, 2003, 22:07:31

Job time : 226 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: June 15, 2003, 22:01:19 ; Search time 64 seconds  
(without alignments)  
694.815 Million cell updates/sec

Title: US-09-884-987-2\_COPY\_175\_319  
Perfect score: 750  
Sequence: 1 GWCLLLPLPIVWKRK.....KANLCTLAEKIQIILKIDT 145

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues  
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+p2n.model -DEV=xlp  
-Q/cgn2\_1/USPTO.spool/US09884987/runat\_09062003\_140301\_13206/app-query.fasta\_1.327  
-DB-Issued Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LISTEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-MODE=LOCAL -OUTFMT=ptc -THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-USER=US09884987 -CGN\_1\_1\_36 -runat\_09062003\_140301\_13206 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=3 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*  
  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750	100.0	920	5	PCT-US95-17083-7
2	750	100.0	1167	5	PCT-US95-17083-1
3	750	100.0	2534	2	US-08-219-237B-1
4	750	100.0	2534	4	US-08-468-560C-1
5	750	100.0	2534	4	US-09-180-100-16
6	750	100.0	2551	4	US-09-230-640-1
7	663	88.4	857	5	PCT-US95-17083-9
8	663	88.4	1104	5	PCT-US95-17083-3
9	663	88.4	2471	1	US-08-444-231-18
10	663	88.4	2471	1	US-08-152-443A-18
11	554.5	73.9	975	5	PCT-US95-17083-5
12	314.5	41.9	1480	4	US-09-230-640-65

Sequence 15, Appl	13	99.5	13.3	257	5	PCT-US95-17083-15
Sequence 149, Appl	14	82	10.9	478	4	US-09-221-017B-149
Sequence 14, Appl	15	81.5	10.9	2288	1	US-08-444-005-14
Sequence 495, Appl	16	78.5	10.5	606	4	US-09-328-111-495
Sequence 1, Appl	17	78.5	10.5	2016	4	US-09-132-118-1
Sequence 16, Appl	18	78.5	10.5	2137	1	US-08-444-005-16
Sequence 1, Appl	19	78.5	10.5	2617	3	US-09-161-443-1
Sequence 2, Appl	20	78.5	10.5	9687	4	US-09-133-944-2
Sequence 2, Appl	21	78.5	10.5	9687	4	US-09-208-827-2
Sequence 626, Appl	22	77.5	10.3	1176	4	US-09-221-017B-626
Sequence 2243, Appl	23	77.5	10.3	11091	4	US-09-134-001C-2243
Sequence 9, Appl	24	76	10.1	3582	2	US-08-400-159-9
Sequence 9, Appl	25	76	10.1	3582	3	US-08-611-729A-9
Sequence 3, Appl	26	73	10.0	1891	4	US-08-973-462-3
Sequence 3, Appl	27	73.5	9.8	1668	4	US-09-813-872-3
Sequence 6, Appl	28	73.5	9.8	2623	3	US-08-804-439A-6
Sequence 6, Appl	29	73.5	9.8	2623	3	US-08-720-229-6
Sequence 2, Appl	30	73.5	9.8	5361	4	US-08-973-462-2
Sequence 1, Appl	31	73.5	9.8	6152	4	US-08-973-462-1
Sequence 1, Appl	32	73.5	9.8	15611	4	US-09-441-340-1
Sequence 17, Appl	33	73	9.7	1186	4	US-09-008-271A-17
Sequence 1, Appl	34	73	9.7	2440	4	US-09-513-007-1
Sequence 2, Appl	35	72.5	9.7	11672	4	US-09-441-340-2
Sequence 5, Appl	36	72	9.6	2465	3	US-08-619-812-5
Sequence 2341, Appl	37	72	9.6	3033	4	US-09-134-001C-2341
Sequence 1838, Appl	38	71.5	9.5	2076	4	US-09-134-001C-1838
Sequence 3, Appl	39	71.5	9.5	2100	4	US-09-134-001C-1217
Sequence 15, Appl	40	71.5	9.5	15567	4	US-09-627-376-3
Sequence 41, Appl	41	71	9.5	1320	1	US-08-257-073-15
Sequence 45, Appl	42	71	9.5	1482	4	US-08-098-327E-41
Sequence 41, Appl	43	71	9.5	1482	4	US-08-098-327E-45
Sequence 45, Appl	44	71	9.5	1482	4	US-08-462-625-41
Sequence 45, Appl	45	71	9.5	1482	4	US-08-462-625-45

ALIGNMENTS

RESULT 1  
PCT-US95-17083-7  
Sequence 7, Application PC/TUS9517083  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
NUMBER OF SEQUENCES: 16  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17083  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/371,263  
FILING DATE: 23-DEC-1994  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 920 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-17083-7

Alignment Scores:  
Pred. No.: 1, 37e-88  
Score: 750.00  
Length: 920  
Percent Similarity: 100.00%  
Matches: 145  
Best Local Similarity: 100.00%  
Conservative: 0  
Query Match: 100.00%  
Mismatch: 0  
Indels: 0  
Caps: 0  
DB: 5

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Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
Db 301 GGGTGGCTTTGCTCTCTCTCTTTCCCAATCCCAATATTCTTTGGGTGAGACAGAGAA 360

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OY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 361 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 420
OY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
DB 421 TTAATCTCCGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATCACC 480
OY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
DB 481 ACTATTGCTGGAGTCATGACATAGCTCAAGTTAAAGGCTTTGTCGAAGAAGATGCTGC 540
OY 81 AsnGluAlaLysIleAspGluLysLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 541 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCTCAAGACACACAGACAGAAA 600
OY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaIleAspThrLeu 120
DB 601 GTTCAACTGCTTGGTAATTGGCATCAACTTTCATGGAAGAAAGAACGCGTATGACACATTG 660
OY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 661 ATTAAGATCTCAAAAAGCCCAATCTTGTACTCTTGACAGAAAATTCAGACTATCATC 720
OY 141 LeuLysAspIleThr 145
DB 721 CTCAGGACATTACT 735

RESULT 2
PCT-US95-17083-1
; Sequence 1, Application PC/TUS9517083
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: SECRETED HUMAN P4S ANTIGEN
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; FILING DATE: PCT/US95/17083
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 23-DEC-1994
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1167 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-17083-1

Alignment Scores:
Pred. No.: 1,948-88 Length: 1167
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x PCT-US95-17083-1 (1-1167)

OY 1 GlyTrpLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20
DB 548 GGGTGGCTTGTCTTCTTTTGGCAATTCACATTAATGTTGGTGAAGAGAAGGAA 607
OY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
DB 608 GTACAGAAACATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATGAATCTCCAACC 667
OY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
DB 668 TTAATCTCCGAACAGTGGCAATAATTTATCTGATGTTGACTTGAGTAAATATATCACC 727
OY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
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DB 728 ACTATTGCTGGAGTCATGACACTAAGTTAAAGGCTTTGTCGAAGAAGATGCTGC 787
OY 81 AsnGluAlaLysIleAspGluLysLysAsnAspValGlnAspThrAlaGluGlnLys 100
DB 788 AATGAAGCCAAATAGATGAGATCAAGATGACATGTCCTCAAGACACACAGACAGAAA 847
OY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaIleAspThrLeu 120
DB 848 GTTCAACTGCTTGGTAATTGGCATCAACTTTCATGGAAGAAAGAACGCGTATGACACATTG 907
OY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
DB 908 ATTAAGATCTCAAAAAGCCCAATCTTGTACTCTTGACAGAAAATTCAGACTATCATC 967
OY 141 LeuLysAspIleThr 145
DB 968 CTCAGGACATTACT 982

RESULT 3
US-08-219-237B-1
; Sequence 1, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; LIBRARY: pCEV4
; CLONE: clone pF58
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 195..1202
; IDENTIFICATION METHOD: by similarity with known sequence or
; IDENTIFICATION METHOD: to an established consensus
; FEATURE:
; NAME/KEY: sig-peptide
; LOCATION: 195..242
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QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 837 TTAATCTGGAACAGTGCATAAATTTATCTGATGTTGACTTGAGTAATAATATACACC 896
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGAAGAATGGTGTC 956
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
Db 957 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACACAGACAGAA 1016
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaIleAspThrLeu 120
Db 1017 GTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGACGGTATGACACATG 1076
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
QY 141 LeuLysAspIleThr 145
Db 1137 CTCAGGACATTACT 1151
RESULT 5
US-09-180-100-16
; Sequence 16, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NO. 630639510
; APPLICANT: NAKAMURA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; EARLIER FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-180-100-16
Alignment Scores:
Pred. No.: 6.09e-88 Length: 2534
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-884-987-2_COPY_175_319 (1-145) x US-09-180-100-16 (1-2534)
QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleValTrpValLysArgLysGlu 20
Db 717 GGGTGGCTTTGCTCTCTTTTGCCTAATTCACCTAATTTGTTGGTGAAGAGAAAGAA 776
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 777 GTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACC 836
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 837 TTAATCTGGAACAGTGCATAAATTTATCTGATGTTGACTTGAGTAATAATATACACC 896
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 897 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGAAGAATGGTGTC 956
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
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Db 957 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAAGACACACAGACAGAA 1016
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaIleAspThrLeu 120
Db 1017 GTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGACGGTATGACACATG 1076
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140
Db 1077 ATTAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAAATTCAGACTATCATC 1136
QY 141 LeuLysAspIleThr 145
Db 1137 CTCAGGACATTACT 1151
RESULT 6
US-09-290-640-1
; Sequence 1, Application US/09290640
; Patent No. 6204055
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPR-0351
; CURRENT APPLICATION NUMBER: US/09/290,640
; CURRENT FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(1228)
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 267
; ISSUE: 15
; PAGES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
US-09-290-640-1
Alignment Scores:
Pred. No.: 6.15e-88 Length: 2551
Score: 750.00 Matches: 145
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-884-987-2_COPY_175_319 (1-145) x US-09-290-640-1 (1-2551)
QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleValTrpValLysArgLysGlu 20
Db 743 GGGTGGCTTTGCTCTCTTTTGCCTAATTCACCTAATTTGTTGGTGAAGAGAAAGAA 802
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40
Db 803 GTACAGAAAACATGCGAAGACACAGAAAGGAAACCAAGGTTCTCATGAATCTCCAACC 862
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60
Db 863 TTAATCTGGAACAGTGCATAAATTTATCTGATGTTGACTTGAGTAATAATATACACC 922
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80
Db 923 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTGCGAAGAATGGTGTC 982
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100
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Db 983 AATGAGCCAAATAGATGAGATCAAGATGACAATCTCCAAAGACACAGCAGACAGAAA 1042  
Qy 101 ValGlnLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120  
Db 1043 GTTCAACTGCTTCGTAATGTCATCAACTTCATGGAAGAAGAGCGTATGACACATG 1102  
Qy 121 IleLysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 140  
Db 1103 ATTAAGATCTCAAAAAGCAATCTTTGACTCTTCAGAGAAAATTCAGACTATCATC 1162  
Qy 141 LeuLysAspIleThr 145  
Db 1163 CTCAAGGACATTACT 1177

RESULT 7  
PCT-US95-17083-9  
; Sequence 9, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 857 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US95-17083-9

Alignment Scores:  
Pred. No.: 2,77e-77 Length: 857  
Score: 663.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.40% Indels: 0  
DB: 5 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x PCT-US95-17083-9 (1-857)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
Db 283 GTGAAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGTTCT 342  
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
Db 343 CATGAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTG 402  
Qy 56 SerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
Db 403 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 462  
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95  
Db 463 CGAAGAATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGAT 522  
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115  
Db 523 ACAGCAGAACAGAAAGTCAACTGCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAA 582  
Qy 116 AlaTyrAspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135  
Db 583 CGGTATGACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTTACTCTTTCAGAGAAA 642  
Qy 136 IleGlnThrIleLeuLysAspIleThr 145  
Db 643 ATTCAAGTATCATCTCTCAAGGACATTACT 672

RESULT 8

PCT-US95-17083-3  
; Sequence 3, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1104 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US95-17083-3

Alignment Scores:  
Pred. No.: 4,02e-77 Length: 1104  
Score: 663.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.40% Indels: 0  
DB: 5 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x PCT-US95-17083-3 (1-1104)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
Db 530 GTGAAGAGAAAGGAGTACAGAAACATGCAGAAAGCAGACAGAAAGGAAACCAAGTTCT 589  
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
Db 590 CATGAATCTCCAACTTAAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTG 649  
Qy 56 SerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
Db 650 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 709  
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95  
Db 710 CGAAGAATGCTGTCATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGAT 769  
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115  
Db 770 ACAGCAGAACAGAAAGTCAACTGCTGTAATTTGGCATCAACTTCAATGGAAGAAAGAA 829  
Qy 116 AlaTyrAspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135  
Db 830 CGGTATGACATGATTAAAGATCTCAAAAAGCCAAATCTTTGTTACTCTTTCAGAGAAA 889  
Qy 136 IleGlnThrIleLeuLysAspIleThr 145  
Db 890 ATTCAAGTATCATCTCTCAAGGACATTACT 919

RESULT 9

US-08-444-231-18  
; Sequence 18, Application US/08444231  
; Patent No. 5652210  
; GENERAL INFORMATION:  
; APPLICANT: BARR, PHILIP J.  
; APPLICANT: SHAPIRO, JOHN P.  
; APPLICANT: KIEFER, MICHAEL C.  
; TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/444,231  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 530  
PRIORITY APPLICATION NUMBER: 08/152,443  
FILING DATE: 15-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: LEHNHARDT, SUSAN K.  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 23647-20006.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2471 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 195..1136  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 243  
US-08-444-231-18

Alignment Scores:  
Pred. No.: 1,32e-76 Length: 2471  
Score: 663.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.40% Indels: 0  
DB: 1 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-08-444-231-18 (1-2471)

QY	16	VallysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer	35
DB	699	GTGAAGAGAAAGAGAGTACGAAACATCGAAGACGACAAAGAAACCAAGGTCT	758
QY	36	HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu	55
DB	759	CATGAATCTCAACCTTAATCTGAACAGTGCATTAATTTATCTGATGTGACTTG	818
QY	56	SerLysTyrlleThrThrleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal	75
DB	819	AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGT	878
QY	76	ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp	95
DB	879	CGAAGAAAGGTGCTAATGAAGCAAAATAGATGAGATCAAGATGACATGCCAAGAC	938
QY	96	ThrAlaGlnGlnLysValGlnLeuLeuArgAsnTriPHisGlnLeuHisGlyLysGlu	115
DB	939	ACAGCAGACAGAAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	998
QY	116	AlaTyAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys	135
DB	999	GGGTATGACACATTTGATTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTGCAGAGAA	1058

QY	136	IleGlnThrIleIleLeuLysAspIleThr	145
DB	1059	ATTCAGACTATCATCTCTCAAGGACATTA	1088
RESULT 10			
US-08-152-443A-18			
Sequence 18, Application US/08152443A			
Patent No. 5663070			
GENERAL INFORMATION:			
APPLICANT: BARR, PHILIP J.			
APPLICANT: SHAPIRO, JOHN P.			
APPLICANT: KIEFER, MICHAEL C.			
TITLE OF INVENTION: NOVEL FAS PROTEIN AND METHODS OF USE			
TITLE OF INVENTION: THEREOF			
NUMBER OF SEQUENCES: 22			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: MORRISON & FOERSTER			
STREET: 755 Page Mill Road			
CITY: Palo Alto			
STATE: California			
COUNTRY: USA			
ZIP: 94304-1018			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: PatentIn Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/152,443A			
FILING DATE: 15-NOV-1993			
CLASSIFICATION: 435			
ATTORNEY/AGENT INFORMATION:			
NAME: LEHNHARDT, SUSAN K.			
REGISTRATION NUMBER: 33,943			
REFERENCE/DOCKET NUMBER: 23647-20006.00			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (415) 813-5600			
TELEFAX: (415) 494-0792			
TELEX: 706141			
INFORMATION FOR SEQ ID NO: 18:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 2471 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 195..1136			
FEATURE:			
NAME/KEY: mat_peptide			
LOCATION: 243			
US-08-152-443A-18			
Alignment Scores:			
Pred. No.: 1,32e-76 Length: 2471			
Score: 663.00 Matches: 130			
Percent Similarity: 100.00% Conservative: 0			
Best Local Similarity: 100.00% Mismatches: 0			
Query Match: 88.40% Indels: 0			
DB: 1 Gaps: 0			
US-09-884-987-2_COPY_175_319 (1-145) x US-08-152-443A-18 (1-2471)			
QY	16	VallysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer	35
DB	699	GTGAAGAGAAAGAGTACGAAACATCGAAGACGACAAAGAAACCAAGGTCT	758
QY	36	HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu	55
DB	759	CATGAATCTCAACCTTAATCTGAACAGTGCATTAATTTATCTGATGTGACTTG	818
QY	56	SerLysTyrlleThrThrleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal	75
DB	819	AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGT	878
QY	76	ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp	95
DB	879	CGAAGAAAGGTGCTAATGAAGCAAAATAGATGAGATCAAGATGACATGCCAAGAC	938
QY	96	ThrAlaGlnGlnLysValGlnLeuLeuArgAsnTriPHisGlnLeuHisGlyLysGlu	115
DB	939	ACAGCAGACAGAAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	998
QY	116	AlaTyAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys	135
DB	999	GGGTATGACACATTTGATTAAGATCTCAAAAAAGCCCAATCTTTGTACTCTTGCAGAGAA	1058



Db 819 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTT 878  
Qy 76 ArglylsasnGlyValasnGluAlaLysIleAspGluIleLysasnAspValGlnAsp 95  
Db 879 CGAAAGAAATGGTCAATGAAGCCAAATAGATGAGATCAAGATGACAAATGTCACAGAC 938  
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGlu 115  
Db 939 ACAGCAGACAGAAAGTCACTGCTCGTAATGGCATCAACTTCATGGAGAAAGAA 998  
Qy 116 AlaTrpAspThrLeuIleLysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLys 135  
Db 999 GCGTATGACACATGATTAAGATCTCAAAAAGCCCAATCTTTGCTACTCTTCAGAGAA 1058  
Qy 136 IleGlnThrIleLeuLysAspIleThr 145  
Db 1059 ATTCAAGACTATCCTCAAGGACATTACT 1088  
RESULT 11  
PCT-US95-17083-5  
; Sequence 5, Application PC/TUS9517083  
; GENERAL INFORMATION:  
; APPLICANT: SECRETED HUMAN FAS ANTIGEN  
; TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/17083  
; FILING DATE: CONCURRENTLY HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/371,263  
; FILING DATE: 23-DEC-1994  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 975 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US95-17083-5  
Alignment Scores:  
Pred. No.: 4,8e-63 Length: 975  
Score: 554.50 Matches: 117  
Percent Similarity: 80.69% Conservative: 0  
Best Local Similarity: 80.69% Mismatches: 1  
Query Match: 73.93% Indels: 28  
DB: 5 Gaps: 1  
US-09-884-987-2\_COPY\_175\_319 (1-145) x PCT-US95-17083-5 (1-975)  
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
Db 439 GGGTGGCTTTGCTCTCTCTTTTGGCAATTCACATAATGTTGGG----- 484  
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
Db 484 ----- 484  
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60  
Db 485 -----CAAACAGTGGCAATAAATTTATCTGATGTTGACITGAGTAAATATATACCC 535  
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
Db 536 ACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTTCCGAAAGAAATGGTGC 595  
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
Db 596 AATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 655  
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120  
Db -----

Db 656 GTTCAACTGCTTCTAATTTGGCATCAACTTCATGGAAGAAAGAGCGTATGACACATTG 715  
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140  
Db 716 ATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCAGAGAAATTCAGACTATCATC 775  
Qy 141 LeuLysAspIleThr 145  
Db 776 CTCAGGACATTACT 790  
RESULT 12  
US-09-290-640-65  
; Sequence 65, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-0351  
; CURRENT APPLICATION NUMBER: US/09/290,640  
; CURRENT FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 65  
; LENGTH: 1480  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (50)..(1033)  
; PUBLICATION INFORMATION:  
; JOURNAL: J. Immunol.  
; VOLUME: 148  
; PAGES: 1274-1297  
; DATE: 1992-02-15  
; DATABASE ACCESSION NUMBER: M83649/Genbank  
; DATABASE ENTRY DATE: 1994-04-18  
US-09-290-640-65  
Alignment Scores:  
Pred. No.: 1.83e-31 Length: 1480  
Score: 314.50 Matches: 69  
Percent Similarity: 66.67% Conservative: 27  
Best Local Similarity: 47.92% Mismatches: 43  
Query Match: 41.93% Indels: 5  
DB: 4 Gaps: 3  
US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-290-640-65 (1-1480)  
Qy 2 Trp---LeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
Db 560 TGGTTGTTGACCATCCTTGTGTTTAAATTCACCTT---GTATTTATATATCGAAAGTAC 616  
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
Db 617 CGGAAAGAAAGTCTGCTGAAAAGGACAGACGATGACCTT-----GAATCTAGAACC 667  
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThrIleThr 60  
Db 668 TCCAGTTCGTGAAACCATACCAATGCAATGCTCAATCTTAGCTTGTAGTAATATACATCCCG 727  
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
Db 728 AGAATTCCTGAAGACATGACAAATCCAGGAAGCTTAAATAATTTGCTCCGAGAAATAACATC 787  
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
Db 788 AAGGAGCGCAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 847  
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120  
Db 848 GTCCAGCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907

QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysLeuGlnThrIleIle 140  
||||| |||||||  
Db 908 ATCAAGGCTCTCAAAAAGCCGAATGTCGAGAACCTTAGATAAAATTCAGGACATGGTC 967  
QY 141 LeuLysAspIle 144  
|||||  
Db 968 CAGAAGGACCTT 979

## RESULT 13

PCT-US95-17083-15  
Sequence 15, Application PC/TUS9517083  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: SECRETED HUMAN FAS ANTIGEN  
NUMBER OF SEQUENCES: 16  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17083  
FILING DATE: CONCURRENTLY HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/371,263  
FILING DATE: 23-DEC-1994  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-17083-15

Alignment Scores:  
Pred. No.: 0.000157 Length: 257  
Score: 99.50 Matches: 22  
Percent Similarity: 55.00% Conservative: 0  
Best Local Similarity: 55.00% Mismatches: 3  
Query Match: 13.27% Indels: 15  
DB: 5 Gaps: 1

US-09-884-987-2\_COPY\_175\_319 (1-145) x PCT-US95-17083-15 (1-257)

QY 1 GlyTrpLeuCysLeuLeuLeuProLeuIleValTrpValLysArgLysGlu 20  
|||||  
Db 158 GGGTGGCTTTGCTCTCTCTTCCCAATTCCTCAATTTGTTGGTGAAG----- 208  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
|||||  
Db 209 -----CTTGGATCCGGAGAGCTCCCAACG 232

## RESULT 14

US-09-221-017B-149/C  
Sequence 149, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: P1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: P2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 149:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 1...478  
US-09-221-017B-149

Alignment Scores:  
Pred. No.: 0.075 Length: 478  
Score: 82.00 Matches: 31  
Percent Similarity: 46.83% Conservative: 28  
Best Local Similarity: 24.60% Mismatches: 45  
Query Match: 10.93% Indels: 22  
DB: 4 Gaps: 5

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-221-017B-149 (1-478)

QY 27 LysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThr--- 45  
|||||  
Db 386 AAGCATGATCGAACAAATCGGACGACTCTAATATCGCGGAGAAATAACAAGAGCGCAAA 327  
QY 46 -----ValAlaIleAsnLeuSerAspValAspLeuSerLysTyr 58  
|||||  
Db 326 CTCTACATCGAGACCTATGGCTGCCAGATGAACGTAGCCGACAGTGGGTG----- 276  
QY 59 IleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsn 78  
|||||  
Db 275 -----GTACGCTCCGTATG-----CAGATGGACGGCTACACCTACCGGAC 234  
QY 79 GlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGlu 98  
|||||  
Db 233 AACGTGGATGAGCGGATACGATCCTGGTCAATACCTGTCGTACGGGACAAATCGCGAG 174  
QY 99 GlnLysVal---GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyr 117  
|||||  
Db 173 CAGAAAGTCTGAACCGGCTGCATATTACCATCTCGTACGAAAGAAAGACGGGCTTCT 114  
QY 118 AspThrLeuLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGln 137  
|||||  
Db 113 TCCCGTCTCTTATCGGGTA-----TTGGGCTGATGTCGCCGAGCGGCTCAAG 66  
QY 138 ThrIleLeuLysAsp 143  
|||||  
Db 65 GAGGAGTTGATCCGCGAA 48

## RESULT 15

US-08-444-005-14  
; Sequence 14, Application US/08444005  
; Patent No. 5674734  
; GENERAL INFORMATION:  
; APPLICANT: Leder, Philip  
; APPLICANT: Seed, Brian  
; APPLICANT: Stanger, Ben Z.  
; APPLICANT: Lee, Tae-Ho  
; APPLICANT: Kim, Emily  
; TITLE OF INVENTION: CELL DEATH PROTEIN  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street, Suite 3100  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,005  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,164  
; REFERENCE/DOCKET NUMBER: 00383/026001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2268 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-444-005-14

Alignment Scores:  
Pred. No.: 0.863 Length: 2268  
Score: 81.50 Matches: 28  
Percent Similarity: 47.87% Conservative: 17  
Best Local Similarity: 29.79% Mismatches: 36  
Query Match: 10.87% Indels: 13  
DB: 1 Gaps: 4

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-08-444-005-14 (1-2268)

Qy	24	ThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnPro	43
Db	1693	ACTTGC-----AAAGAGAGCTCGACTCCAGACACCAAGCCACTTTGTGATAAC---	1740
Qy	44	GluthrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThrThrIleAla	63
Db	1741	-----ACCACCTAGCTGACTGATGACACCTGAACCCCTATCAGGGAACCTGGGA	1791
Qy	64	GlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAla	83
Db	1792	-----AGGCAGCTGAAAAAAGTGCCTCCAGAGCTGGCTTCACCTGAGTCT	1836
Qy	84	LysIleAspGluIleLysAsnAspAsnValClnAspThrAlaGluGlnLysVal---	102
Db	1837	CAGATCGAATGAAATCGACCATGACTATCAAGAGCTGAGCTGAAAGAGAAAGTTTACCA	1896
Qy	103	LeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAla	116

Db 1897 ATGCTTCAGAAAGTGGCTGATCGGGAAGGACCAAAAGGGGCC 1938  
Search completed: June 15, 2003, 22:59:24  
Job time : 69 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 15, 2003, 22:33:24 ; Search time 130 Seconds  
(without alignments)  
1615.145 Million cell updates/sec

Title: US-09-884-987-2\_COPY\_175\_319

Perfect score: 750

Sequence: 1 GWICLLLLPIPLIVWKRKE.....KANLCTLAERKIQFIILKDIIT 145

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q/cgn2\_1/USPTO.spool/US0984987/runat\_09062003\_140302\_13292/app\_query.fasta.1.327.  
-DB=PublishedApplications\_NA -QFMT=fastap -SUFFIX=p2n.rnp -MINMATCH=0.1.  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosom62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US0984987 -ECGN\_1\_1\_104\_erunat\_09062003\_140302\_13292  
-NCPU=6 -ICPU=3 -NO\_MAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PublishedApplications\_NA:\*\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*\*
- 11: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*\*
- 12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*\*
- 14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	750	100.0	2534	10	US-09-949-713-16
2	750	100.0	2534	10	US-09-884-987-1
3	750	100.0	2551	10	US-09-802-669-1
4	750	100.0	8282	9	US-09-966-976A-7

Alignment Scores:			
Pred. No.:	2,79e-87	Length:	2534
Score:	750.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

ALIGNMENTS

RESULT 1  
US-09-949-713-16  
; Sequence 16, Application US/09949713  
; Patent No. US20020044944A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAMURA, No. US20020044944A110  
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
; FILE REFERENCE: 1110-207P  
; CURRENT APPLICATION NUMBER: US/09/949,713  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US/09/180,100  
; PRIOR FILING DATE: 1998-11-02  
; PRIOR APPLICATION NUMBER: PCT/JP97/01502  
; PRIOR FILING DATE: 1997-05-01  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 2534  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-949-713-16

Sequence 7, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 102, App  
Sequence 17113, A  
Sequence 2490, Ap  
Sequence 3156, Ap  
Sequence 998, App  
Sequence 101, App  
Sequence 13045, A  
Sequence 15171, A  
Sequence 7395, Ap  
Sequence 65, Appl  
Sequence 99, Appl  
Sequence 98, Appl  
Sequence 919, App  
Sequence 218, Appl  
Sequence 6140, Ap  
Sequence 6140, Ap  
Sequence 495, App  
Sequence 1, Appli  
Sequence 15, Appl  
Sequence 13, Appl  
Sequence 103, App  
Sequence 138, App  
Sequence 138, App  
Sequence 647, Appl  
Sequence 6, Appli  
Sequence 14730, A  
Sequence 4, Appli  
Sequence 1804, Ap  
Sequence 188, App  
Sequence 20550, A  
Sequence 3784, Ap  
Sequence 8513, Ap  
Sequence 7040, Ap  
Sequence 3000, Ap  
Sequence 1, Appli  
Sequence 1464, Ap  
Sequence 29, Appl  
Sequence 2, Appli

Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-09-884-987-2_COPY_175_319 (1-145) x US-09-949-713-16 (1-2534)			
Qy 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeulleValTrpValLysArgLysGlu 20			
Db 717 GGGTGGCTTGTGCTCTCTCTTTTGCCAAATCCACTAATGTTTGGGTGAAGAGAAAGAA 776			
Qy 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40			
Db 777 GTACAGAAACATCTCAGAAAGCAGAGAAAGAAACCCAGGTTCTCATGAATCTCCAACC 836			
Qy 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr 60			
Db 837 TTAATCTCTGAACAGTGGCAATAAATTTATCTCATGTTGACTTGAGTAAATATATCACC 896			
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80			
Db 897 ACTATTCTGGAGTCATGAGCACTAAGTCAAGTTAAAGGCTTGTGTCAAAGAATGGTGTC 956			
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100			
Db 957 AATGAACCCAAATAGATGAGATCAACAAATGACAAATGTCCAAGACACAGACAGACAGAA 1016			
Qy 101 ValGlnLeuLeuArgAsnThrPHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu 120			
Db 1017 GTTCAACTGCTTCGTAAATTGGCATCAACTTCATGTGAAGAAGAAGCGTATGACACATTG 1076			
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140			
Db 1077 ATTAAGATCTCAAAAAGCCAACTCTTGTACTCTTCACAGAGAAAATTCAGACTATTCATC 1136			
Qy 141 LeuLysAspIleThr 145			
Db 1137 CTCAAGGACATTACT 1151			

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RESULT 2
US-09-884-987-1
; Sequence 1, Application US/09884987
; Patent No. US20020102653A1
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu et al.
; TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE ANTIGEN
; FILE REFERENCE: 0020-4877P
; CURRENT APPLICATION NUMBER: US/09/884,987
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: (1831)..(1836)
; NAME/KEY: mat_peptide
; LOCATION: (243)..()
; NAME/KEY: sig_peptide
; LOCATION: (195)..(242)
; NAME/KEY: CDS
; LOCATION: (195)..(1199)
; NAME/KEY: polyA_site
; LOCATION: (2352)..(2357)
; NAME/KEY: polyA_site
; LOCATION: (2518)..(2532)
US-09-884-987-1

Alignment Scores:      2.79e-87
Pred. No.:             2534
Score:                  750.00
Percent Similarity:     100.00%
Best Local Similarity:  100.00%
Mismatches:              0

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Query Match:	100.00%	Indels:	0
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Qy	1	GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu	20
Db	717	GGG7GGCTTTGTC7TCTCTTTTGCCAAATCCACTAATGTGTTGGGTGAAGAGAAAGAA	776
Qy	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40
Db	777	GTACGAAACATCTCAGAAAGACAGAAAGAAACCAGGCTTCTCATGAATCTCCAAACC	836
Qy	41	LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrIleThr	60
Db	837	TTAAATCCTGAAACAGTGGCAATAAATTTATCTCATGTGACTGAATAATATATCACC	896
Qy	61	ThrIleAlaGlyValMetThrLeuSerSerGlnValLysGlyPheValArgLysAsnGlyVal	80
Db	897	ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTGTGAAAGAATGGTGTC	956
Qy	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100
Db	957	AATGAACCCAAATAGATGAGATCAAGATGACAAATGCAATGCTCCAGNCACAGCAGAACACAGAA	1016
Qy	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaTyrAspThrLeu	120
Db	1017	GTTCAACTGCTTCGTAAATTGGCATCAACTTCATGTGAAAGAAGAAGCGTATGACACATTG	1076
Qy	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
Db	1077	ATTAAGATCTCAAAAAGGCCAATCTTTGTACTCTTCACAGAGAAAATTCAGACTATCATC	1136
Qy	141	LeuLysAspIleThr	145
Db	1137	CTCAAGGACATTACT	1151

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RESULT 3
US-09-802-669-1
; Sequence 1, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussou, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (221)..(1228)
; PUBLICATION INFORMATION:
; JOURNAL: J. Biol. Chem.
; VOLUME: 267
; ISSUE: 15
; PAGES: 10709-10715
; DATE: 1992-05-25
; DATABASE ACCESSION NUMBER: X63717/Genbank
; DATABASE ENTRY DATE: 1996-07-19
US-09-802-669-1

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US-09-802-669-1

Query Match:	100.00%	Indels:	0
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QY	1	GlyTrpLeuCysLeuLeuLeuProLeuLeuValTrpValLysArgLysGlu	20
Db	4401	GGGTGGCTTTCCTCTCTTTCCCAATCCACTAAATTGTTGGGTGAAGAAAGGAA	4342
QY	21	ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr	40
Db	4341	GTACAGAAAACATGCAGAAAGCAGAGAAGAAACCAGGTTCTCATGAATCTCCAACC	4282
QY	41	LeuasnProGluThrValAlaIleasLeuSeraspValaspLeuSerLysIleThr	60
Db	4281	TTAATCTCGAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATCAC	4222
QY	61	ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValargLysAsnGlyVal	80
Db	4221	ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTGTGTCAAAGAATGGTGT	4162
QY	81	AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys	100
Db	4161	AATCAAGCCAAATAGATGAGATCAAGATGACAATGCCATTCATGTTGAAAGAATGGTGC	4102
QY	101	ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyraSphThrLeu	120
Db	4101	GTTCAACTGCTGCTAATTGGCATCAACTTCATGTTGAAAGAAGCGTATGACACATTG	4042
QY	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle	140
Db	4041	ATTAAAGATCTCAAAAAGGCAATCTTTGTACTCTTTCAGAGAGAAAAATTCAGACTATCAT	3982
QY	141	LeuLysAspIleThr 145	
Db	3981	CTCAAGGACATTACT 3967	
 RESULT 5			
; Sequence 7, Application US/09963206B			
; Patent No. US20020123076A1			
; GENERAL INFORMATION:			
; APPLICANT: Ferrick, David A.			
; APPLICANT: Swift, Susan E.			
; APPLICANT: Fox, Bryan			
; TITLE OF INVENTION: Methods and Compositions for Screening for Modulators and			
; FILE OF INVENTION: Secretion and Switch Rearrangement			
; CURRENT APPLICATION NUMBER: US/09/963,206B			
; CURRENT FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US 09/076,624			
; PRIOR FILING DATE: 1998-05-12			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 7			
; LENGTH: 8282			
; TYPE: DNA			
; ORGANISM: Artificial sequence			
; FEATURE:			
; OTHER INFORMATION: synthetic			
US-09-963-206B-7			
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Pred. No.:	1,61e-86	Length:	8282
Score:	750.00	Matches:	145
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
 US-09-884-987-2_COPY_175_319 (1-145) x US-09-963-206B-7 (1-8282)			

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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 8345
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-09-966-976A-8

Alignment Scores:
  1.62e-86
Score: 750.00
Length: 8345
Matches: 145
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0
DB: 9

US-09-884-987-2_COPY_175_319 (1-145) x US-09-966-976A-8 (1-8345)

QY 1 GlyTTPLeuCysLeuLeuLeuProileProLeuIleValTrpValLysArgLysGlu 20
Db 4401 GGGTGGCTTGTCTCTCTTTTGGCAATTCACATAATTGTTGGGTGAAGAGAAGGAA 4342
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40

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US-09-963-206B-8

Alignment Scores:
Pred. No.:      1,62e-86      Length:      8345
Score:          750.00      Matches:      145
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             10      Gaps:         0

US-09-884-987-2_COPY1_75_319 (1-145) x US-09-963-206B-8 (1-8345)

QY      1 GlyTrpLeuCySLeuLeuLeuLeuProIleProLeuIleValTrpvallySargLySGLu 20
|||||
DB      4401 GGGTGGCTTGTGCTCTCTCTTTTGGCAATTCACAAATTTGGTGGAGAGAAAGGAA 4342

QY      21 ValGlnLysThrCysargLysHisargLySGLuAsnGlnLySerHisGluSerProThr 40
|||||
DB      4341 GTACAGAAACCATGCAGAAAGCACAGAAAGAAACCAAGGTTCTCATCAATCTCCAACC 4282

QY      41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerlySyrIleThr 60
|||||

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Db 4281 TTAATCCTGAAACAGCTGGCAATAAATTTATCTGATGTTGACCTTGAATTAATATATACAC 4222  
Qy 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValargLysAsnGlyVal 80  
Db 4221 ACTATTGCTGGAGTCATGACACAACTCAAGTAAAGGGTTTGTTCGAAGAATGTTGTC 4162  
Qy 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
Db 4161 AATGAAGCCAAATAGATGATGATCAAGATGACAATGTCCAGACACAGCAGAACAGAAA 4102  
Qy 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrrAspThrLeu 120  
Db 4101 GTTCAACTGCTTGGTAATTGGCATCAACTTCATGGAAAGAAAGACGATGACACATTG 4042  
Qy 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleIle 140  
Db 4041 ATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAAATTCAGACTATCATC 3982  
Qy 141 LeuLysAspIleThr 145  
Db 3981 CTCAGGACATTACT 3967

## RESULT 8

US-09-802-669-102  
; Sequence 102, Application US/09802669  
; Patent No. US2002004490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/230,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 102  
; LENGTH: 836  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(399)  
US-09-802-669-102

Alignment Scores:  
Pred. No.: 1,12e-76 Length: 836  
Score: 663.00 Matches: 130  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 88.40% Indels: 0  
DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-802-669-102 (1-836)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
Db 396 GTCAGAGAAAGGAGTACAGAAACATGTCAGAGACAGAAAGAAACCAAGGTCT 455  
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
Db 456 CATGAATCTCAACCTTAATCTGAAACAGTGCATTAATTTATCTGATGTTGACTTG 515  
Qy 56 SerLysTyrrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
Db 516 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 575  
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95

Db 576 CGAAAGAATGGTCTCAATCAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGAC 635  
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115  
Db 636 ACAGCAGAACAGAAAGTTCAACTGCTTGCATAATTGGCATCAACTTTCATGGAAGAAAGAA 695  
Qy 116 AlaTyrrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135  
Db 696 GCGATATGACACATTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCGACAGAAA 755  
Qy 136 IleGlnThrIleIleLeuLysAspIleThr 145  
Db 756 ATTCACTATCATCTCTCAAGGACATTACT 785

## RESULT 9

US-09-918-995-17119  
; Sequence 17119, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17119  
; LENGTH: 490  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.Feature  
; LOCATION: (1)...(490)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-17119

Alignment Scores:  
Pred. No.: 2.96e-70 Length: 490  
Score: 611.00 Matches: 125  
Percent Similarity: 96.92% Conservative: 1  
Best Local Similarity: 96.15% Mismatches: 4  
Query Match: 81.47% Indels: 1  
DB: 9 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-918-995-17119 (1-490)

Qy 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
Db 60 GTCAGAGAAAGGAGTACAGAAACATGTCAT-TTGCACAGAAATGAAACCAAGGCTCT 118  
Qy 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
Db 119 CATGAATCTCAACCTTAGATCTCTGAAACAGACAGCAATAAATTTATCTGATGTTGACTTG 178  
Qy 56 SerLysTyrrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
Db 179 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTT 238  
Qy 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95  
Db 239 CGAAAGAATGGTCTCAATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAAGAC 298  
Qy 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115  
Db 299 ACAGCAGAACAGAAAGTGCATCTTCGTAATTTGGCATCACTTTCATGGAAGAAAGAA 358  
Qy 116 AlaTyrrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135  
Db 359 GCGTATGACACATTGATTAAAGATCTCAAAAAGCCAAATCTTTGTACTCTTCGACAGAAA 418

QY 136 lleGlnThrIleleuLysAspIleThr 145  
|||||  
Db 419 ATTGAGACTATCATCTCAAGCACATTACT 448

## RESULT 10

US-09-867-701-2490  
; Sequence 2490, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2490  
; LENGTH: 398  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(398)  
; OTHER INFORMATION: n - A,T,C or G  
US-09-867-701-2490

Alignment Scores:  
Pred. No.: 4,34e-69 Length: 398  
Score: 601.00 Matches: 118  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 80.13% Indels: 0  
DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-867-701-2490 (1-398)

QY 28 HisArgLysGluAsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAla 47  
|||||  
Db 3 CACAGAAAGGAAACCAAGGTTCTCATGAATCTCAACCTTAAATCTCTGAACAGTGCA 62  
QY 48 lleAsnLeuSerAspValAspLeuSerLysThrIleThrIleAlaGlyValMetThr 67  
|||||  
Db 63 ATAAATTTATCTGATGTTGACTTGAGTAATATATATCACTATTCCTGGAGTCATGACA 122  
QY 68 LeuSerGlnValLysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGlu 87  
|||||  
Db 123 CTAGTCAAGTTAAAGGCTTTGTTCCGAAAGAAATGGTGTCATGAAGCCAAATAGATCAG 182  
QY 88 lleLysAsnAspAsnValGlnAspThrIleGlnLysValGlnLeuLeuArgAsnTrp 107  
|||||  
Db 183 ATCAAGATGACATGTCACAGACACAGACAGAAAGTTCAACTGCTCGTAATGG 242  
QY 108 HisGlnLeuHisGlyLysGluAlaThrAspThrLeuLysAspLeuLysLysAla 127  
|||||  
Db 243 CATCACTTCATGAAAGAAAGACGCTATGACACATTTGATTAAGATCTCAAAAAGCC 302  
QY 128 AsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeuLysAspIleThr 145  
|||||  
Db 303 AATCTTTCTACTCTGCAGAGAAATTCAGACTATCATCTCAAGGACATTACT 356

## RESULT 11

US-09-867-701-3156  
; Sequence 3156, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Jones, Robert  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3156  
; LENGTH: 460  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-867-701-3156

## Alignment Scores:

Pred. No.: 1,92e-64 Length: 460  
Score: 566.00 Matches: 112  
Percent Similarity: 99.12% Conservative: 1  
Best Local Similarity: 98.25% Mismatches: 1  
Query Match: 75.47% Indels: 0  
DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-867-701-3156 (1-460)

QY 32 AsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSer 51  
|||||  
Db 1 AACCAAGGTTCTCATGAATCTCAACCTTAAATCTGAAACAGTGGCAATTAATTTACT 60  
QY 52 AspValAspLeuSerLysThrIleThrIleAlaGlyValMetThrLeuSerGlnVal 71  
|||||  
Db 61 GATGTTGACTTTCAGTAATATATATCACTATTCCTGGAGTCATGACACTAAGTCAAGTT 120  
QY 72 LysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGluLysAsnAsp 91  
|||||  
Db 121 AAAGCTTTGTTGGAAGAAAGTGTCAATGAAGCCAAATAGATGATCAAGATGAC 180  
QY 92 AsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHis 111  
|||||  
Db 181 AATGTCCAAGACACAGCAGACAGAAAGTTCAACTGCTTCGTAATTCGATCACTTCAT 240  
QY 112 GlyLysLysGluAlaThrAspThrLeuLysAspLeuLysLysLysLysLysLys 131  
|||||  
Db 241 GGAAGAAATTAATCGATGACACATTTGATTAAGATCTCAAAAAGCCAAATTTGTACT 300  
QY 132 LeuAlaGluLysIleGlnThrIleLeuLysAspIleThr 145  
|||||  
Db 301 CTTCGAGAGAAATTCAGACTATCATCTCAAGGACATTACT 342

## RESULT 12

US-09-954-531-998  
; Sequence 998, Application US/09954531  
; Patent No. US20020165180A1  
; GENERAL INFORMATION:  
; APPLICANT: Weaver, Zoe  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using  
; FILE REFERENCE: 689290-77  
; CURRENT APPLICATION NUMBER: US/09/954,531  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: US/60/233,133  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,009  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,034  
; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,509  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: US/60/234,567  
; PRIOR FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 1392  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 998  
; LENGTH: 975  
; TYPE: DNA  
; ORGANISM: Homo sapiens

## US-09-954-531-998

Alignment Scores:  
Pred. No.: 1,836-62 Length: 975  
Score: 554.50 Matches: 117  
Percent Similarity: 80.69% Conservatives: 0  
Best Local Similarity: 80.69% Mismatches: 1  
Query Match: 73.93% Indels: 28  
DB: 9 Gaps: 1

## US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-954-531-998 (1-975)

QY 1 GlyTyrLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu.20  
DB 439 GGGTGGCTTGCTCTCTTTTGGCAATCCACATTAATGTTTGGG-----484  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
DB 484 -----484  
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysThr 60  
DB 485 -----GAAACAGTGGCAATAAATTTATCTGATGTTGACTTGAGTAAATATATACCC 535  
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
DB 536 ACTATTGCTGGAGTCATGACATGACATGACATGACATGACATGACATGACATGACATG 595  
QY 81 AsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLys 100  
DB 596 AATGAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 655  
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeu 120  
DB 656 GTTCACTGCTCGTAATGGATCACTCACTCACTCACTCACTCACTCACTCACTCACTG 715  
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140  
DB 716 ATTAAGATCTCAAAAGCCCAATCTTGTACTCTTGCAGAGAAATTCAGACTATCATC 775  
QY 141 LeuLysAspIleThr 145  
DB 776 CTCAGGACATTAAT 790

## RESULT 13

US-09-802-669-101  
; Sequence 101, Application US/09802669  
; Patent No. US2002004490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcussen, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 09/665,615  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US 09/290,640  
; PRIOR FILING DATE: 1999-04-12  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 101  
; LENGTH: 1840  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (95)...(426)  
US-09-802-669-101

## Alignment Scores:

Pred. No.: 2,05e-50 Length: 1840  
Score: 465.00 Matches: 92  
Percent Similarity: 97.89% Conservatives: 1  
Best Local Similarity: 96.84% Mismatches: 2  
Query Match: 62.00% Indels: 0  
DB: 10 Gaps: 0

## US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-802-669-101 (1-1840)

QY 51 SerAspValAspLeuSerLysThrIleThrIleAlaGlyValMetThrLeuSerGln 70  
DB 91 TCAGATGTTGACTTGTGTAATATATATACCACTATTGCTGGAGTCATGTCATATGTCAA 150  
QY 71 ValLysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGluLysAsn 90  
DB 151 GTTAAAGCGCTTGTTCGAAAGAAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGAAT 210  
QY 91 AspAsnValGlnAspThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeu 110  
DB 211 GACATGTCAGACACACACAGACAGAAAGTTCAACTGCTTCGTAAATGGCATCACTT 270  
QY 111 HisGlyLysGluAlaTrpAspThrLeuLysIleLysAspLeuLysLysAlaAsnLeuCys 130  
DB 271 CATGGAAGAAAGAGCGGTATGACACATTTGATTAAAGATCTCAAAAGCCAAATCTTTGT 330  
QY 131 ThrLeuAlaGluLysIleGlnThrIleIleLeuLysAspIleThr 145  
DB 331 ACTCTTGCAGAGAAATTCAGACTATCATCTCCTCAAGGACATTAAT 375

## RESULT 14

US-09-918-995-13045  
; Sequence 13045, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13045  
; LENGTH: 489  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(489)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-918-995-13045

## Alignment Scores:

Pred. No.: 4.6e-46 Length: 489  
Score: 425.00 Matches: 84  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 56.67% Indels: 0  
DB: 9 Gaps: 0

## US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-918-995-13045 (1-489)

QY 62 IleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsn 81  
DB 57 ATTGCTGGAGTCATGACACTAGTCAAGTTAAAGGCTTTGTTGCAAGAAATGGTGTCAAT 116  
QY 82 GluAlaLysIleAspGluLysAsnAspValGlnAspThrAlaGluGlnLysVal 101  
DB 117 GAAGCCAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 176  
QY 102 GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTrpAspThrLeuIle 121

```

Db      177 CAACGCTTCGTAATGGCATCACTTCATGGAAGAAGACGCGTATGACACATTGATT 236
QY      122 LysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 141
Db      237 AAGATCTCAAAAAGCCAACTTTGTACTCTTCGAGAGAAAATTTCAGACTATCATCCTC 296
QY      142 LysAspIleThr 145
Db      297 AAGGACATTACT 308

```

RESULT 15

```

US-09-918-995-15171
; Sequence 15171, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hysseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38034
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15171
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(496)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-15171

```

Alignment Scores:

```

Pred. No.:      4.7e-46      Length:      496
Score:          425.00      Matches:      84
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      56.67%      Indels:      0
DB:              9          Gaps:      0

```

US-09-884-987-2\_COPY\_175\_319 (1-145) x US-09-918-995-15171 (1-496)

```

QY      62 IleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyValAsn 81
Db      65 ATTGCTGGAGTCATGACACTAAGTCAAGTTAAGGCTTTGTCGAAAGAATGGTGTCAAT 124
QY      82 GluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLysVal 101
Db      125 GAAGCCAAATAGATGAGATCAAGATGACATGTCCAGACACAGCAGACAGAAAGTT 184
QY      102 GlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrAspThrLeuIle 121
Db      185 CAACGCTTCGTAATGGCATCACTTCATGGAAGAAGACGCGTATGACACATTGATT 244
QY      122 LysAspLeuLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIleLeu 141
Db      245 AAGATCTCAAAAAGCCAACTTTGTACTCTTCGAGAGAAAATTTCAGACTATCATCCTC 304
QY      142 LysAspIleThr 145
Db      305 AAGGACATTACT 316

```

Search completed: June 15, 2003, 23:50:14  
Job time : 139 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: June 15, 2003, 21:50:09; Search time 1418 Seconds  
(without alignments)  
1656.097 Million cell updates/sec

Title: US-09-884-987-2\_COPY\_175\_319  
Perfect score: 750  
Sequence: 1 GNLCLLLPLPIVWKRRE.....KANLCTLAEXIQTIILKDIY 145

Scoring table:  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q/cgn2\_1/USPTO.spool/US09884987/runat\_09062003\_140300\_13188/app\_query.fasta\_1.327  
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-UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45  
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-OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MMALP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_etc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_etc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_othr:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	750	100.0	1055	14	BQ051037 AGENCOURT
2	699	93.2	417	10	AV651157
3	663	88.4	509	10	AW994695 RCI-BN003
4	656.5	87.5	776	13	BI254532 602978522
5	644.5	85.9	809	12	BF126149 601650407
6	618	82.4	676	14	W05802 za89f05.r1
7	606.5	80.9	395	10	BE070451 QV4-BF040
8	601	80.1	398	9	AA180032 zo93g12.r
9	566	75.5	460	9	AA293570 zt25h11.r
10	495	66.0	305	9	AA860068 HGBBT125
11	492	65.6	1152	14	BM922638 AGENCOURT
12	426	56.8	696	10	AV715411
13	375	50.0	932	9	AL542093
14	337	44.9	217	9	AA852070 HGBBT116
15	314.5	41.9	1437	11	AK002590 Mus muscu
16	293	39.1	735	13	BI766250 603052708
17	280	37.3	663	10	AW141748 EST291827
18	215	28.7	461	14	H02935 yj46b08.r1
19	205	27.3	954	9	AA745982 ob18g12.s
20	200	26.7	827	9	AJ392468 AJ392468
21	155	20.7	1052	13	BM455788 AGENCOURT
22	149	19.9	828	13	BI838027
23	135.5	18.1	494	12	BF718215
24	135.5	18.1	577	12	BF717834
25	99	13.2	577	12	BG512043
26	92.5	12.3	562	10	AV383635
27	91	12.1	562	13	BM540069
28	89.5	11.9	683	10	AV852164
29	89	11.9	394	14	BM880215
30	88.5	11.8	543	14	BM793563
31	88.5	11.8	553	14	BQ488484
32	88.5	11.8	716	10	AV383642
33	88.5	11.8	796	10	AV383307
34	88.5	11.8	1042	17	CNS05EYH
35	88	11.7	688	14	BQ240549
36	87.5	11.7	1026	17	BH147298
37	87	11.6	584	9	AI231531
38	87	11.6	998	17	CNS07A5F
39	86	11.5	653	14	BQ285491
40	85.5	11.4	495	13	BJ411502
41	84.5	11.3	701	14	BQ510872
42	84.5	11.3	851	17	AZ681486
43	84	11.2	410	9	AI950629
44	83.5	11.1	611	12	BG794187
45	83.5	11.1	699	9	AJ448187

ALIGNMENTS

RESULT 1  
BQ051037  
LOCUS BQ051037 1055 bp mRNA linear EST 29-MAR-2002  
DEFINITION AGENCOURT\_6954504 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:5785846  
5', mRNA sequence.  
ACCESSION BQ051037  
VERSION BQ051037.1 GI:19810377  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1055)  
NTH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM12873 row: j column: 23  
High quality sequence stop: 589.

FEATURES  
source

Location/Qualifiers  
1. 1055  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5785846"  
/clone\_lib="NIH\_MGC\_71"  
/tissue\_type="leiomyosarcoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb."  
352 a 221 c 215 g 267 t

BASE COUNT  
ORIGIN

## Alignment Scores:

Pred. No.: 6,61e-80 Length: 1055  
Score: 750.00 Matches: 145  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x BQ051037 (1-1055)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
DB 326 GGGTGGCTTTGCTCTCTCTTTTGGCCAAATCCCACTAATCTTTGGGTGAAGAGAAAGAA 385  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
DB 386 GTACAGAAACATGCGAAGAGACAGAGAAAGAAAGCAAGGTTCTCATGTAATCTCCAACT 445  
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrlleThr 60  
DB 446 TTAATCTCGACACATGCGCAATATATCTGTGTTGACCTGAGTAATATATATATATATAT 505  
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
DB 506 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAATGGTGTG 565  
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
DB 566 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAGACACAGCAGACAGAA 625  
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrlleThrLeu 120  
DB 626 GTTCAACTGCTGCTGTAATGGCATCACTCATGGAAGAAAGACGGTATGACATG 685  
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIle 140  
DB 686 ATTAAGATCTCAAAAGCCAACTTTGTACTCTTTCAGAGAAATTCAGACTATCATC 745  
QY 141 LeuLysAspIleThr 145  
DB 746 CTCAGGACATTACT 760

## RESULT 2

AV6511157  
LOCUS AV6511157 417 bp mRNA linear EST 15-JAN-2002  
DEFINITION AV6511157 GLC Homo sapiens cDNA clone GLCCMD03 3', mRNA sequence.  
ACCESSION AV6511157

VERSION  
KEYWORDS  
SOURCE

AV6511157.1 GI:9872171  
EST.  
human.

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 417)  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Xiao.H., Qu.J., Liu.F., Huang.Q., Cheng.Z., Li.N., Du.J., Hu.W., Shen.K., Lu.G., Fu.G., Zhong.M., Xu.S., Gu.W., Huang.W., Zhao.X., Hu.G., Gu.J., Chen.Z. and Han.Z.

## AUTHORS

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver  
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

## TITLE

Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919(ex. 45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

JOURNAL  
MEDLINE  
COMMENT

21625106  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
Tel: 86-21-50801919(ex. 45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn  
This clone is available at CHGC in Shanghai.

## FEATURES

## source

Location/Qualifiers  
1. 417  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="GLCCMD03"  
/clone\_lib="GLC"  
/tissue\_type="corresponding non cancerous liver tissue"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 151 a 74 c 84 g 108 t  
ORIGIN

## Alignment Scores:

Pred. No.: 2,66e-74 Length: 417  
Score: 699.00 Matches: 134  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.20% Indels: 0  
DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AV651157 (1-417)

QY 1 GlyTrpLeuCysLeuLeuLeuProIleProLeuIleValTrpValLysArgLysGlu 20  
DB 16 GGGTGGCTTTGCTCTCTCTTTTGGCCAAATCCCACTAATCTTTGGGTGAAGAGAAAGAA 75  
QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProThr 40  
DB 76 GTACAGAAACATGCGAAGAGACAGAGAAAGAAAGCAAGGTTCTCATGTAATCTCCAACT 135  
QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTyrlleThr 60  
DB 136 TTAATCTCGCAACATGCGCAATATATCTGTGTTGACCTGAGTAATATATATATATATAT 195  
QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
DB 196 ACTATTGCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCAAAGAAATGGTGTG 255  
QY 81 AsnGluAlaLysIleAspGluIleLysAsnAspValGlnAspThrAlaGluGlnLys 100  
DB 256 AATGAAGCCAAATAGATGAGATCAAGATGACAATGTCCAGACACAGCAGACAGAA 315  
QY 101 ValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysGluAlaTyrlleThrLeu 120  
DB 316 GTTCAACTGCTGCTGTAATGGCATCACTCATGGAAGAAAGACGGTATGACATG 375  
QY 121 IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGlu 134

```

|||||
376 ATTAAGATCTCAAAAGGCAATCTTTGTACCTTCAGAG 417

RESULT 3
LOCUS      AW994695
DEFINITION R01-BN0039-060200-011-a05 BN0039 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW994695
VERSION     AW994695.1 GI:8254929
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 509)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
             M.J., Soares,F., Brentani,R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE     20203663
COMMENT     Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-RC1-BN0039-060
             200-011-a05&t3=2000-02-06&t4=1)
             Seq primer: puc 18 forward
             High quality sequence stop: 509.
FEATURES
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        1..509
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="BN0039"
            /dev_stage="Adult"
            /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters' Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the puc 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT  205 a 83 c 99 g 122 t
ORIGIN
Alignment Scores:
Pred. No.: 7.64e-70 Length: 509
Score: 663.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.40% Indels: 0
DB: 10 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x AW994695 (1-509)

QY 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35
Db ||||||
14 GTGAAGAGAGAGGAGTACAGAAACATGTCAGAAAGCAGAAAGCAAGGTTCT 73
QY 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55
Db ||||||
74 CATGAATCTCCAACTTAAATCCTGAAACAGTGCATATAAATTTATCTGATGTTGACTTG 133

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---

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QY 56 SerLysTyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75
Db ||||||
134 AGTAAATATATACCACTATTGCTGGAGTCATGACACTAAGTCAAGTAAAGGCTTTGTT 193

QY 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAsp 95
Db ||||||
194 CGAAGAAATGCTCATGATGAGCCAAATAGATGAGATCAAGATGACATGTCACAGAC 253

QY 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHisGlyLysLysGlu 115
Db ||||||
254 ACAGCAGACAGAAAGTTCAACTGCTTCGTAATTTGGCATCAACTTCATGGAAGAAAGAA 313

QY 116 AlaTyrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLys 135
Db ||||||
314 GCGTATGACACATTGATTAAAGATCTCAAAAAGCCCAATCTTTGTACTCTTGCAGAGAA 373

QY 136 IleGlnThrIleIleLeuLysAspIleThr 145
Db ||||||
374 ATTCACTATCATCTCTCAAGGACATTACT 403

RESULT 4
BI254532 776 bp mRNA linear EST I7-JUL-2001
LOCUS      602978522F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5123477 5',
DEFINITION mRNA sequence.
ACCESSION  BI254532
VERSION     BI254532.1 GI:14807044
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 776)
AUTHORS     NIH-MGC http://mgi.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
             Email: cgapps-remail.nih.gov
             Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: LLAM1301 row: 1 column: 06
             High quality sequence stop: 757.
FEATURES
    source
        1..776
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="NIH_MGC_12"
            /tissue_type="cervical carcinoma cell line"
            /lab_host="DH10B"
            /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
            Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.4 kb. Library prepared by Life
            Technologies."
BASE COUNT  276 a 136 c 151 g 213 t
ORIGIN
Alignment Scores:
Pred. No.: 8.22e-69 Length: 776
Score: 656.50 Matches: 141
Percent Similarity: 96.58% Conservative: 0
Best Local Similarity: 96.58% Mismatches: 4
Query Match: 87.53% Indels: 4
DB: 13 Gaps: 0

US-09-884-987-2_COPY_175_319 (1-145) x BI254532 (1-776)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProIleProLeuValTrpValLysArgLysGlu 20

```

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

BASE COUNT	293 a	127 c	179 g	210 t
ORIGIN				
Alignment Scores:				
Pred. No.:	2	44e-67	Length:	809
Score:	644.50		Matches:	140
Percent Similarity:	97.24%		Conservative:	1
Best Local Similarity:	96.55%		Mismatches:	4
Query Match:	85.93%		Indels:	4
DB:	12		Gaps:	0

US-09-884-987-2 COPY 175 319 (1-145) x BF1261149 (1-809)

81 AsnGluAlaLysIleAspGluIleLysAsnAspAsnValGlnAspThrAlaGluGlnLys 100  
 |||||  
 278 AATGAAGCCAAATAGATGAGATCAAGATGCAATGTCCACAGACACAGCAGACAGAAA 337  
 |||||  
 101 ValGlnIleuAraAsnTroHisGlnIleuHisGluIleValGluAlaIleAspThrIleu 120

Db	338	GTTCACCTGCTTCGTAATTGGCATCAACTTCTGAAAGAAAGACGGTATCACACATG -	396
	121	IleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleGlnThrIlelle	140
QY			
	397	ATTAAGATCTCAAAAAAGCCAACTCTTGTACTCTTGACAGAAAAATTCAGACTATCATC	456
Db			

ORGANISM	HOMO SAPIENS
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 676) Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu



This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: mob.REGA+ET  
High quality sequence stop: 307.

## FEATURES

source

Location/Qualifiers

1. 676  
/organism="Homo sapiens"  
/db\_xref="GDB:124466"  
/db\_xref="taxon:9606"  
/clone="IMAGE:299745"  
/clone\_lib="Soares\_fetal\_lung\_NBHL19W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: p773D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTTTTTTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

231 a 127 C 138 G 171 T 9 others  
BASE COUNT  
ORIGIN

## Alignment Scores:

Pred. No.: 3e-64 Length: 676  
Score: 618.00 Matches: 126  
Percent Similarity: 96.92% Conservative: 0  
Best Local Similarity: 96.92% Mismatches: 2  
Query Match: 82.40% Indels: 2  
DB: 14 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x W05802 (1-676)

QY 18 ArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGlu 37  
Db 17 AGAAAGGAAGTACAGAAACATGCGAGNAGCAGAGAAAGAAACCAAGGTTCTCATGAA 76  
QY 38 SerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLys 57  
Db 77 TCTCAACCTTAAATCCTGGAACAGTGGCAATAAATTTATCTGATGTTGAGTGAATA 136  
QY 58 TyrIleThrThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal-Argly 77  
Db 137 TATATCACCACCTATGTTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGTTCCGAA 196  
QY 77 sAsnGlyValAsnGluAlaLysIleAspGluLysAsnAspValGlnAspThrAl 97  
Db 137 GAATGGTGTCAATGAAGCCAAATAGATGAGATCAAGATGCAATGTTCCAAAGACACAGC 256  
QY 97 aGluGlnLysValGlnLeuLeu-ArgAsnTrpHisGlnLeuHisGlyLysLysGluAlaT 117  
Db 257 AGAACAGAAAGTTCACCTGCTTCCGTAATGTCATCAACTTCATGGAAGAAAGAGCGT 316  
QY 117 yrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThrLeuAlaGluLysIleG 137  
Db 317 ATGACACATGATTAAGATCTCAAAAAGCCAAATCTTTGTACTCTTGCAGAGAAATTC 376  
QY 137 InThrIleLeuLysAspIleThr 145  
Db 377 AGACTATCATCTCAAGGACATTACT 402

## RESULT 7

BE070451/c

LOCUS

DEFINITION

QV4-BT0407-020300-122-d09 BT0407 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BE070451

VERSION

BE070451.1

KEYWORDS

EST.

## SOURCE

ORGANISM

REFERENCE

AUTHORS

COMMENT

TITLE

JOURNAL

MEDLINE

CONTACT

CONTACT

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Db 144 AATGAGCCAAATAGATGAGATCAGATGCAATGCAATGTCCTCAAGACACAGACAGACAGAA 85  
 QY 101 ValGlnLeuLeuA:GASnTrPHISGlnLeuHisGlyLysGluAla---TyrAspThr 119  
 Db 84 GTTCAACTGCTTCGTAATTGTCATCAACTTTTAAACACGGGAAAGTAGTAGACACA 25  
 QY 120 LeuilelyAspLeuLys 125  
 Db 24 TTGATTAAAGATCTCAAA 7

RESULT 8  
 AAL180032  
 LOCUS  
 DEFINITION zo3932.r1 Stratagene ovarian cancer (#937219) Homo sapiens CDNA  
 clone IMAGE:594502 5' similar to gb:M67454 FASL RECEPTOR PRECURSOR  
 (HUMAN);, mRNA sequence.  
 ACCESSION AAL180032  
 VERSION AAL180032.1 GI:1761298  
 KEYWORDS EST..  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 398)  
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins  
 , M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore  
 , B., Mullis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
 TITLE Generation and analysis of 280,000 human expressed sequence tags  
 JOURNAL Genom Res. 6 (9), 807-828 (1996)  
 MEDLINE 97044478  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estewatson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 263.

FEATURES  
 source Location/Qualifiers  
 1..398  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="IMAGE:594502"  
 /clone\_lib="Stratagene ovarian cancer (#937219)"  
 /sex="female"  
 /dev\_stage="adult, 64 years"  
 /lab\_host="SOLR (kanamycin resistant)"  
 /notes="Vector: Bluescript SK-; Site 1: ECORI; Site 2: XhoI  
 ; Cloned unidirectionally. Primer: Oligo dT. Papillary  
 serous carcinoma, isolated from ascites, 64 year old  
 caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector;  
 -5' adaptor sequence: 5' GAATTCGCACGAG 3' -3' adaptor  
 sequence: 5' CTCGAGTTTTTTTTTTTTT 3"  
 BASE COUNT 155 a 73 c 73 g 96 t 1 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1,64e-62 Length: 398  
 Score: 601.00 Matches: 118  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 80.13% Indels: 0  
 DB: 9 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AAL180032 (1-398)  
 QY 28 HisAtgLySGluAsnGInGlySerHisGluSerProThrLeuAsnProGluThrValAla 47

the Not-I and Eco RI sites of a modified pT7n3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo.

BASE COUNT 175 a 80 c 81 g 124 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3,32e-58 Length: 460  
Score: 566.00 Matches: 112  
Percent Similarity: 99.12% Conservative: 1  
Best Local Similarity: 98.25% Mismatches: 1  
Query Match: 75.47% Indels: 0  
DB: 9 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AA293570 (1-460)

QY 32 AsnGlnGlySerHisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSer 51  
DB 1 AACCAAGGTTCTCATGAATCTCCAACTTAATCTGGAACAGTGGCAATAATTTATCT 60  
QY 52 AspValAspLeuSerLysTyrIleThrIleAlaGlyValMetThrLeuSerGlnVal 71  
DB 61 GATGTGACTTGGTAAATATATATACCACTATTCTGGAGTCATGACACATAAGTCAAGTT 120  
QY 72 LysGlyPheValArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAsp 91  
DB 121 AAAGGCTTTGTCGAAGAAGTGGTCAATGAAGCCAAATAGATGAGATCAAGATGAC 180  
QY 92 AsnValGlnAspThrAlaGluGlnLysValGlnLeuArgAsnTrpHisGlnLeuHis 111  
DB 181 ATGTCCAGACACACAGCAGCAAGAAAGTTCACCTGCTTAATGGCATCACTTCAT 240  
QY 112 GlyLysLysGluAlaTyrAspThrLeuIleLysAspLeuLysLysAlaAsnLeuCysThr 131  
DB 241 GGAAGAAATAATCGTATCATCATCATGATTAAGATCTCAAAAAGCCCAATCTTTGTACT 300  
QY 132 LeuAlaGluLysIleGlnThrIleLeuLysAspIleThr 145  
DB 301 CTTGCGAGAGAAATTCAGACTATCATCTCCTCAAGGACATTACT 342

RESULT 10  
LOCUS AA860068 305 bp mRNA linear EST 11-MAR-1998  
DEFINITION HGBT125 Human Glioblastoma Cell Homo sapiens cDNA, mRNA sequence.  
ACCESSION AA860068  
VERSION AA860068.1 GI:2952547  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 305)  
AUTHORS Jin, H.L., Hu, S.N., Tu, C., Yuan, J.G. and Qiang, B.O.  
TITLE DDRT-PCR of Human Glioblastoma Cell Line BT-325 CDNAs  
JOURNAL Unpublished (1997)  
COMMENT Contact: Boqin Qiang  
National Laboratory of Medical Molecular Biology, CAMS & PUMC  
Institute of Basic Medical Sciences, Peking Union Medical College &  
Chinese Academy of Medical Sciences  
5 Dong Dan San Tiao, Beijing 100005, P.R. China  
Tel: (010)65236411  
Fax: 8610-5240529  
Email: zh357@iname.com

Seq primer: M13 Reverse Primer.  
FEATURES  
Location/Qualifiers  
1..305  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Human Glioblastoma Cell"  
/cell\_type="Glioblastoma Cell"  
/cell\_line="BT-325"  
/lab\_host="E.coli DH5a"  
/note="Organ: Brain; Vector: PCR11, Invitrogen; Total RNA

was isolated from human glioblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and sequenced.

BASE COUNT 122 a 52 c 64 g 67 t  
ORIGIN

Alignment Scores:  
Pred. No.: 6.93e-50 Length: 305  
Score: 495.00 Matches: 96  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 66.00% Indels: 0  
DB: 9 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AA860068 (1-305)

QY 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
DB 17 GTGAAGAGAAAGAGTACAGAAACATGCAGAAAGCAGAAAGGAAACCAAGGTTCT 76  
QY 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
DB 77 CATGATCTCCAACTTAATCTGGAACAGTGGCAATAATTTATCTGATGTTGACTTG 136  
QY 56 SerLysTyrIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
DB 137 ACTAAATATATACCACTATTCTGGAGTCATGACACTAAGTCAAGTTAAAGGCTTTGT 196  
QY 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95  
DB 197 CGAAGAAGTGGTCAATGAAGCCAAATAGATGATCAAGATCAAGATGACAAATGCTCAAGAC 256  
QY 96 ThrAlaGluGlnLysValGlnLeuLeuArgAsnTrpHisGlnLeuHis 111  
DB 257 ACAGCAGAACAGAAAGTTCATCTGCTTAATGGCATCACTTCAT 304

RESULT 11

LOCUS BM922638

DEFINITION AGENCOURT\_6652776 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5755724

ACCESSION 5', mRNA sequence.

VERSION BM922638

KEYWORDS BM922638.1 GI:19373017

SOURCE EST.

human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1152)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@remail.nih.gov](mailto:cgapsb@remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12795 row: c column: 21  
High quality sequence start: 52  
High quality sequence stop: 628.

FEATURES

Location/Qualifiers

1..1152

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:5755724"

/clone\_lib="NIH\_MGC\_118"

/tissue\_type="leukocyte"

BASE COUNT 354 a 273 c 276 g 249 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 9,66e-49 Length: 1152  
 Score: 492.00 Matches: 109  
 Percent Similarity: 88.37% Conservatives: 5  
 Best Local Similarity: 84.50% Mismatches: 10  
 Query Match: 65.60% Indels: 5  
 DB: 14 Gaps: 2

US-09-884-987-2\_COPY\_175\_319 (1-145) x BM922638 (1-1152)

QY 16 ValLysArgLysGluValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySer 35  
 |||||  
 Db 467 GTGAAGAGAAAGGAAGTACAGAAACATGCAGAAAGCACAGAAAGCAACCAAGGTTCT 526

QY 36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
 |||||  
 Db 527 CATGAATCTCAACCTTAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACCTG 586

QY 56 SerLysTrpIleThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheVal 75  
 |||||  
 Db 587 AGTAATATATACACATATTGCTGGAGTCAATGACATTAAGTCAAGTAAAGGCTTTGTT 646

QY 76 ArgLysAsnGlyValAsnGluAlaLysIleAspGluIleLysAsnAspValGlnAsp 95  
 |||||  
 Db 647 CGAAAGAGTGTGTCAATGGAGCCAAATAGATGATGATCAAGATGACAATGTCCAGAC 706

QY 96 ThrAlaGluGlnLysValGlnLeuArgAsnTrpHisGlnLeuHisGlyLys---L 114  
 |||||  
 Db 707 CCAGCAGAAAGAGAAGTTCACCTCTTCCAAATGGGCATCAACTTCATGGGAAGGAA 766

QY 114 ysgLualatyAspThrLeu-IleLysAspLeuLysAla---AsnLeuCysThrLeu 132  
 |||||  
 Db 767 AGAAGCGTATGACACCTTGGATTAAAGATCTCCAAAGAGCCCAACCTTGGACCTCTG 826

QY 133 AlaGluLysIleGlnThrIle 139  
 |||||  
 Db 827 GCGAAGAAATTCAGAACTA 847

RESULT 12  
 AV715411  
 LOCUS AV715411 DCB Homo sapiens cDNA clone DCBAUC01 5', mRNA sequence. EST 11-OCT-2000  
 DEFINITION AV715411  
 ACCESSION AV715411  
 VERSION AV715411.1 GI:10796928  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 696)  
 AUTHORS Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,  
 Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,  
 Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu  
 G., Cheng,Z. and Han,Z.  
 TITLE Homo sapiens cDNA DCB clones  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China

FEATURES  
 source  
 1..696  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="DCBAUC01"  
 /clone\_lib="DCB"  
 /cell\_type="dendritic cells"  
 /dev\_stage="mature"  
 /lab\_host="BM25\_8"  
 /note="Vector: pTriplex2; Site\_1: sfiIA; Site\_2: sfiIB"

BASE COUNT 210 a 141 c 156 g 189 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4,44e-41 Length: 696  
 Score: 426.00 Matches: 82  
 Percent Similarity: 98.82% Conservatives: 2  
 Best Local Similarity: 96.47% Mismatches: 1  
 Query Match: 56.80% Indels: 0  
 DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AV715411 (1-696)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProLeuProLeuIleValTrpValLysArgLysGlu 20  
 |||||  
 Db 430 GGGTGGCTTGTCT 489

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProthr 40  
 |||||  
 Db 490 GTACAGAAACATGCAGAAAGCACAGAAAGCAAGGAAACCAAGGTTCTCATGAATCTCCAACC 549

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60  
 |||||  
 Db 550 TTAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTCAGTAAATATATATCACC 609

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
 |||||  
 Db 610 ACTATGCTGGAGTCAATGACACTAAAGTCAAGCTTTGTTTCAAGAAATGGTGTGTC 669

QY 81 AsnGluAlaLysIle 85  
 |||||  
 Db 670 ATTGAAGCCCAACTG 684

RESULT 13  
 AL542093  
 LOCUS AL542093 LTI\_FL002\_PL1 Homo sapiens cDNA clone CS0DE009Y106 5 prime  
 DEFINITION AL542093 932 bp mRNA linear EST 16-FEB-2001  
 ACCESSION AL542093  
 VERSION AL542093.1 GI:12873796  
 KEYWORDS EST.  
 SOURCE human.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 932)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequenage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES  
 source  
 1..932  
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 /db\_xref="taxon:9606"  
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 /clone\_lib="LTI\_FL002\_PL1"

FEATURES  
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 /clone\_lib="DCB"  
 /cell\_type="dendritic cells"  
 /dev\_stage="mature"  
 /lab\_host="BM25\_8"  
 /note="Vector: pTriplex2; Site\_1: sfiIA; Site\_2: sfiIB"

BASE COUNT 210 a 141 c 156 g 189 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 4,44e-41 Length: 696  
 Score: 426.00 Matches: 82  
 Percent Similarity: 98.82% Conservatives: 2  
 Best Local Similarity: 96.47% Mismatches: 1  
 Query Match: 56.80% Indels: 0  
 DB: 10 Gaps: 0

US-09-884-987-2\_COPY\_175\_319 (1-145) x AV715411 (1-696)

QY 1 GlyTrpLeuCysLeuLeuLeuLeuProLeuProLeuIleValTrpValLysArgLysGlu 20  
 |||||  
 Db 430 GGGTGGCTTGTCT 489

QY 21 ValGlnLysThrCysArgLysHisArgLysGluAsnGlnGlySerHisGluSerProthr 40  
 |||||  
 Db 490 GTACAGAAACATGCAGAAAGCACAGAAAGCAAGGAAACCAAGGTTCTCATGAATCTCCAACC 549

QY 41 LeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeuSerLysTrpIleThr 60  
 |||||  
 Db 550 TTAATCTCTGAAACAGTGGCAATTAATTTATCTGATGTTGACTTCAGTAAATATATATCACC 609

QY 61 ThrIleAlaGlyValMetThrLeuSerGlnValLysGlyPheValArgLysAsnGlyVal 80  
 |||||  
 Db 610 ACTATGCTGGAGTCAATGACACTAAAGTCAAGCTTTGTTTCAAGAAATGGTGTGTC 669

QY 81 AsnGluAlaLysIle 85  
 |||||  
 Db 670 ATTGAAGCCCAACTG 684

was isolated from human glioblastoma cell line BT325. Then Differential Display RT-PCR was conducted between normal and all-trans Retinoic Acid induced cell. Differentially expressed PCR products were cloned and sequenced.

BASE COUNT	86 a	34 c	48 g	49 t
ORIGIN				

Percent Similarity: 100.00%      Conservative: 1

DB: 9 Gaps: 0

36 HisGluSerProThrLeuAsnProGluThrValAlaIleAsnLeuSerAspValAspLeu 55  
77 CATGAATCTCCAACTTAAATCTCTGAACAGTGGCAATAAATTTACTGATGTTGACCTTG 136

77 CATGAATCTTCAACCTTAATCTGAAACAGTGGCAATAAATTATCTGATGTTGACTTG 136

137 AGTAAATATATCACCACCTATTGTGGAGTCATGACACTAAGTCAAGTTAAAGCTTTGTT 196

Db 197 CGAAGAATGGTGCAATGAA, 217

Accession	LOCUS	DEFINITION	Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:061001D23:tumor necrosis factor receptor	1437 bp	mRNA	linear	HTC 19-JAN-2000
AK002590	AK002590						

ACCESSION	AK002590
VERSION	AK002590.1 GI:12832683
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male kidney cDNA to mRNA, clone:lib-RIKEN full-length enriched mouse cDNA library clone:0610012D23.
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

REFERENCE	1
AUTHORS	Carlinici, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2

AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3

**AUTHORS**  
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujitake, S., Inoue, K., Todawa, I., Izawa, M., Ohara, E., Watanishi, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kiria, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system—384-format  
sequencing pipeline with 384 multicapillary sequencer

**TITLE**



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